GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 18:14:26 ; Search time 134 Seconds
(without alignments)
116.836 Million cell updates/sec

Title: US-10-723-368-5
Perfect score: 254
Sequence: 1 TQAQLLRVGCVLGTCQVQNL.....MGPAGRQDSAPVDPSSPHSY 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	254	100.0	47	17	US-10-850-055-14	Sequence 14, Appl
2	72.5	28.5	52	9	US-09-813-345-14	Sequence 14, Appl
3	72.5	28.5	52	14	US-10-197-954-2	Sequence 2, Appli
4	72.5	28.5	52	16	US-10-474-635A-19	Sequence 19, Appl
5	72.5	28.5	52	17	US-10-718-071-43	Sequence 43, Appl
6	72.5	28.5	52	17	US-10-760-085-2	Sequence 2, Appli
7	72.5	28.5	185	15	US-10-364-889-6	Sequence 6, Appli
8	72.5	28.5	185	15	US-10-372-683-12	Sequence 12, Appl
9	72.5	28.5	185	16	US-10-675-406A-7	Sequence 7, Appli
10	72.5	28.5	185	16	US-10-755-889-148	Sequence 148, App
11	69.5	27.4	50	9	US-09-813-345-15	Sequence 15, Appl
12	68.5	27.0	52	17	US-10-718-071-16	Sequence 16, Appl
13	64	25.2	103	15	US-10-264-237-1622	Sequence 1622, Ap
14	63.5	25.0	216	16	US-10-437-963-198108	Sequence 198108,
15	62.5	24.6	52	15	US-10-360-101-74	Sequence 74, Appl
16	59	23.2	142	15	US-10-307-817-14	Sequence 14, Appl
17	58.5	23.0	92	16	US-10-437-963-198935	Sequence 198935,
18	58.5	23.0	521	16	US-10-437-963-124602	Sequence 124602,
19	58.5	23.0	576	15	US-10-184-648-26	Sequence 26, Appl
20	58	22.8	560	14	US-10-238-129-8	Sequence 8, Appli
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22	58	22.8	1544	15	US-10-369-493-6078	Sequence 6078, Ap
23	57	22.4	117	16	US-10-767-701-51114	Sequence 51114, A
24	56.5	22.2	575	15	US-10-425-114-64569	Sequence 64569, A
25	56	22.0	89	16	US-10-437-963-136207	Sequence 136207,
26	56	22.0	107	9	US-09-764-870-356	Sequence 356, App
27	56	22.0	107	9	US-09-764-853-470	Sequence 470, App
28	56	22.0	107	14	US-10-125-540-356	Sequence 356, App
29	56	22.0	107	14	US-10-103-313-301	Sequence 301, App
30	56	22.0	107	15	US-10-158-057-335	Sequence 335, App
31	56	22.0	947	15	US-10-461-194-114	Sequence 114, App
32	55	21.7	220	16	US-10-767-701-32051	Sequence 32051, A
33	55	21.7	322	15	US-10-424-599-175411	Sequence 175411,
34	55	21.7	669	15	US-10-120-801-108	Sequence 108, App
35	54.5	21.5	126	16	US-10-437-963-202043	Sequence 202043,
36	54.5	21.5	320	16	US-10-437-963-119917	Sequence 119917,
37	54.5	21.5	751	16	US-10-437-963-135754	Sequence 135754,
38	54	21.3	538	16	US-10-437-963-151317	Sequence 151317,
39	53.5	21.1	135	15	US-10-264-049-4093	Sequence 4093, Ap
40	53.5	21.1	303	14	US-10-097-340-143	Sequence 143, App
41	53.5	21.1	303	14	US-10-171-311-87	Sequence 87, Appl
42	53.5	21.1	329	10	US-09-999-121-6	Sequence 6, Appli
43	53	20.9	86	9	US-09-864-761-48541	Sequence 48541, A
44	53	20.9	117	10	US-09-789-390-41	Sequence 41, Appl
45	53	20.9	136	14	US-10-156-761-8699	Sequence 8699, Ap

ALIGNMENTS

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RESULT 1
US-10-850-055-14
; Sequence 14, Application US/10850055
; Publication No. US20050009742A1
; GENERAL INFORMATION:
;  APPLICANT: Bertilsson, Goran
;  APPLICANT:  Erlandsson, Rikard
;  APPLICANT:  Frisen, Jonas
;  APPLICANT:  Haegerstrand, Anders
;  APPLICANT:  Heidrich, Jessica
;  APPLICANT:  Hellstrom, Kristina
;  APPLICANT:  Haggblad, Johan
;  APPLICANT:  Jansson, Katarina
;  APPLICANT:  Kortesman, Jarkko
;  APPLICANT:  Lindquist, Per
;  APPLICANT:  Lundh, Hanna
;  APPLICANT:  McGuire, Jacqueline
;  APPLICANT:  Mercer, Alex
;  APPLICANT:  Nyberg, Karl
;  APPLICANT:  Ossoinak, Amina
;  APPLICANT:  Patrone, Cesare
;  APPLICANT:  Ronnholm, Harriet
;  APPLICANT:  Wikstrom, Lillian
;  APPLICANT:  Zachrisson, Olof
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS
;  FILE REFERENCE: 21882-517 CIP
;  CURRENT APPLICATION NUMBER: US/10/850,055
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 10/718,071
;  PRIOR FILING DATE: 2003-11-20
;  PRIOR APPLICATION NUMBER: US 60/427,912
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 47
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-850-055-14

  Query Match             100.0%;  Score 254;  DB 17;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-25;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47


RESULT 2
US-09-813-345-14
; Sequence 14, Application US/09813345
; Patent No. US20020068814A1
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Derek D.
;                   Saha, Shankar
;                   Abel, Peter W.
;        TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;                            SUPERFAMILY AND METHODS OF USE
;        NUMBER OF SEQUENCES: 23
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;             STREET: 119 No. US20020068814A1th Fourth Street
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/813,345
;             FILING DATE: 20-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McCormack, Myra H
;             REGISTRATION NUMBER: 36,602
;             REFERENCE/DOCKET NUMBER: 180.00020101
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612/305-1220
;             TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 52 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-813-345-14

  Query Match             28.5%;  Score 72.5;  DB 9;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.067;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
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Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 3
US-10-197-954-2
; Sequence 2, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
;  APPLICANT: K"ster, Hubert
;  APPLICANT:  Siddiqi, Suhaib
;  APPLICANT:  Little, Daniel
;  TITLE OF INVENTION: Capture Compounds, Collections Thereof
;  TITLE OF INVENTION:  And Methods For Analyzing The Proteome And Complex
;  TITLE OF INVENTION:  Compositions
;  FILE REFERENCE: 24743-2305
;  CURRENT APPLICATION NUMBER: US/10/197,954
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 60/306,019
;  PRIOR FILING DATE: 2001-07-16
;  PRIOR APPLICATION NUMBER: 60/314,123
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: 60/363,433
;  PRIOR FILING DATE: 2002-03-11
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-197-954-2

  Query Match             28.5%;  Score 72.5;  DB 14;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.067;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
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Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 4
US-10-474-635A-19
; Sequence 19, Application US/10474635A
; Publication No. US20040176567A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Innovation Ltd
;  TITLE OF INVENTION: Peptides
;  FILE REFERENCE: 480821.00004
;  CURRENT APPLICATION NUMBER: US/10/474,635A
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: GB 0109438.2
;  PRIOR FILING DATE: 2001-04-17
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-474-635A-19

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  Best Local Similarity   38.5%;  Pred. No. 0.067;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
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Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


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US-10-718-071-43
; Sequence 43, Application US/10718071
; Publication No. US20050009847A1
; GENERAL INFORMATION:
;  APPLICANT: Bertilson, Goran
;  APPLICANT:  Erlandsson, Rikard
;  APPLICANT:  Frisen, Jonas
;  APPLICANT:  Haegerstrand, Anders
;  APPLICANT:  Heidrich, Jessica
;  APPLICANT:  Hellstrom, Kristina
;  APPLICANT:  Haggblad, Johan
;  APPLICANT:  Jannson, Katarina
;  APPLICANT:  Kortesmaa, Jarkko
```

```
;  APPLICANT:  Lindquist, Per
;  APPLICANT:  Lundh, Hanna
;  APPLICANT:  Mcguire, Jacqueline
;  APPLICANT:  Mercer, Alex
;  APPLICANT:  Nyberg, Karl
;  APPLICANT:  Ossoinak, Amina
;  APPLICANT:  Patrone, Cesare
;  APPLICANT:  Ronnholm, Harriet
;  APPLICANT:  Wirkstrom, Lilian
;  APPLICANT:  Zachrisson, Olof
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS
;  FILE REFERENCE: 21882-517 UTIL
;  CURRENT APPLICATION NUMBER: US/10/718,071
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: US 60/427,912
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-071-43

  Query Match            28.5%;  Score 72.5;  DB 17;  Length 52;
  Best Local Similarity  38.5%;  Pred. No. 0.067;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

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RESULT 6
US-10-760-085-2
; Sequence 2, Application US/10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
;  APPLICANT: Hubert K"ster
;  APPLICANT:  Daniel Paul Little
;  APPLICANT:  Suhaib Mahmood Siddiqi
;  APPLICANT:  Mattew Peter Grealish
;  APPLICANT:  Subramaniam Marappan
;  APPLICANT:  Chester Frederick Hassman III
;  APPLICANT:  Ping Yip
;  TITLE OF INVENTION: Capture Compounds, Collections Thereof
;  TITLE OF INVENTION:  And Methods For Analyzing The Proteome And Complex
;  TITLE OF INVENTION:  Compositions
;  FILE REFERENCE: 24743-2309
;  CURRENT APPLICATION NUMBER: US/10/760,085
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: 60/441,398
;  PRIOR FILING DATE: 2003-01-16
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-760-085-2

  Query Match            28.5%;  Score 72.5;  DB 17;  Length 52;
  Best Local Similarity  38.5%;  Pred. No. 0.067;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 7
US-10-364-889-6
; Sequence 6, Application US/10364889
; Publication No. US20030224989A1
; GENERAL INFORMATION:
;  APPLICANT: Pahel, Gregory L.
;  APPLICANT:  Quinn, Kerry
;  TITLE OF INVENTION: Compositions and Methods for Treatment of Osteoarthritis
;  FILE REFERENCE: 21402-558
;  CURRENT APPLICATION NUMBER: US/10/364,889
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: 60/356,376
;  PRIOR FILING DATE: 2002-02-12
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-889-6

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  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

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RESULT 8
US-10-372-683-12
; Sequence 12, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.
;  APPLICANT:  PEALE JR., FRANKLIN V.
;  APPLICANT:  WU, THOMAS D.
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
;  FILE REFERENCE: P1928R1P1
;  CURRENT APPLICATION NUMBER: US/10/372,683
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 10/271,690
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/344,534
;  PRIOR FILING DATE: 2001-10-18
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 12
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-372-683-12

  Query Match            28.5%;  Score 72.5;  DB 15;  Length 185;
  Best Local Similarity  38.5%;  Pred. No. 0.27;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
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Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146


RESULT 9
US-10-675-406A-7
; Sequence 7, Application US/10675406A
; Publication No. US20040121375A1
; GENERAL INFORMATION:
;  APPLICANT: Bayer Pharmaceuticals Corporation
;  APPLICANT:  Eveleigh, Deepa
;  APPLICANT:  Taylor, Ian
;  TITLE OF INVENTION: METHODS FOR PREDICTION AND PROGNOSIS OF CANCER, AND MONITORING
;  TITLE OF INVENTION:  CANCER THERAPY
;  FILE REFERENCE: 5138
;  CURRENT APPLICATION NUMBER: US/10/675,406A
;  CURRENT FILING DATE:  2003-09-30
;  PRIOR APPLICATION NUMBER: US 60/415,194
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;  PRIOR FILING DATE: 2002-09-30
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-675-406A-7

  Query Match             28.5%;  Score 72.5;  DB 16;  Length 185;
  Best Local Similarity   38.5%;  Pred. No. 0.27;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
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Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146


RESULT 10
US-10-755-889-148
; Sequence 148, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
;  TITLE OF INVENTION:  PATHWAY
;  FILE REFERENCE: D0284 NP
;  CURRENT APPLICATION NUMBER: US/10/755,889
;  CURRENT FILING DATE:  2004-01-13
;  PRIOR APPLICATION NUMBER: U.S. 60/440,068
;  PRIOR FILING DATE: 2003-01-14
;  PRIOR APPLICATION NUMBER: U.S. 60/469,757
;  PRIOR FILING DATE: 2003-05-12
;  NUMBER OF SEQ ID NOS: 823
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-755-889-148

  Query Match             28.5%;  Score 72.5;  DB 16;  Length 185;
  Best Local Similarity   38.5%;  Pred. No. 0.27;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146


RESULT 11
US-09-813-345-15
; Sequence 15, Application US/09813345
; Patent No. US20020068814A1
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Derek D.
;                   Saha, Shankar
;                   Abel, Peter W.
;        TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;                            SUPERFAMILY AND METHODS OF USE
;        NUMBER OF SEQUENCES: 23
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;             STREET: 119 No. US20020068814A1th Fourth Street
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/813,345
;             FILING DATE: 20-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McCormack, Myra H
;             REGISTRATION NUMBER: 36,602
;             REFERENCE/DOCKET NUMBER: 180.00020101
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612/305-1220
;             TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 50 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-813-345-15

  Query Match             27.4%;  Score 69.5;  DB 9;  Length 50;
  Best Local Similarity   35.9%;  Pred. No. 0.16;
  Matches   14;  Conservative    7;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| :| |:|:::|      :   || :  ||  |
Db         13 GCRFGTCTMQKLAHQIYQFT-DKDKDGMAPRNKISPQGY 50


RESULT 12
US-10-718-071-16
; Sequence 16, Application US/10718071
; Publication No. US20050009847A1
; GENERAL INFORMATION:
;  APPLICANT: Bertilson, Goran
;  APPLICANT:  Erlandsson, Rikard
;  APPLICANT:  Frisen, Jonas
;  APPLICANT:  Haegerstrand, Anders
;  APPLICANT:  Heidrich, Jessica
;  APPLICANT:  Hellstrom, Kristina
;  APPLICANT:  Haggblad, Johan
;  APPLICANT:  Jannson, Katarina
;  APPLICANT:  Kortesmaa, Jarkko
;  APPLICANT:  Lindquist, Per
;  APPLICANT:  Lundh, Hanna
;  APPLICANT:  Mcguire, Jacqueline
;  APPLICANT:  Mercer, Alex
;  APPLICANT:  Nyberg, Karl
;  APPLICANT:  Ossoinak, Amina
;  APPLICANT:  Patrone, Cesare
;  APPLICANT:  Ronnholm, Harriet
;  APPLICANT:  Wirkstrom, Lilian
;  APPLICANT:  Zachrisson, Olof
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS
;  FILE REFERENCE: 21882-517 UTIL
;  CURRENT APPLICATION NUMBER: US/10/718,071
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: US 60/427,912
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-071-16

  Query Match             27.0%;  Score 68.5;  DB 17;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.22;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
```

```
              ||  ||| || |:|:: |      : : ||    ||  |
Db          15 GCRFGTCTVQKLAHQITQFT-DKDKDNVAPRSKISPQGY 52
```

RESULT 13
US-10-264-237-1622
; Sequence 1622, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1622
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (62)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1622

```
  Query Match             25.2%;  Score 64;  DB 15;  Length 103;
  Best Local Similarity   40.0%;  Pred. No. 1.8;
  Matches   18;  Conservative    5;  Mismatches   14;  Indels    8;  Gaps    3;

Qy          2 QAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHS 46
              |||||  ||   | :   :|  | ::||       :|| ||||
Db          8 QAQLLDSGC-QQTSPLDPDNHNAW-ILGPPS------LDPRSPHS 44
```

RESULT 14
US-10-437-963-198108
; Sequence 198108, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198108
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_93800C.1.pep
US-10-437-963-198108

```
  Query Match             25.0%;  Score 63.5;  DB 16;  Length 216;
  Best Local Similarity   31.0%;  Pred. No. 4.7;
  Matches   13;  Conservative   13;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 LRVGCVLGTCQVQNLSHR-----LWQLMGPAGRQDSAPVDPS 42
              | :| ::|||:| ::|:      : :: |   |: :| :|||
Db         19 LGLGIIIGTCEVTSVSNERLGFAVNRVHGGGSRKQTAEIDPS 60
```

RESULT 15
US-10-360-101-74
; Sequence 74, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A13,S16-sequence of Adrenomedullin Hypotensive peptide
US-10-360-101-74

```
  Query Match             24.6%;  Score 62.5;  DB 15;  Length 52;
  Best Local Similarity   35.9%;  Pred. No. 1.4;
  Matches   14;  Conservative    6;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              |   ||| || |:|:::|      : : ||    ||  |
Db         15 GSRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52
```

Search completed: May 4, 2005, 18:27:15
Job time : 135 secs

OM protein - protein search, using sw model

Run on: May 4, 2005, 17:56:39 ; Search time 162 Seconds
(without alignments)
112.208 Million cell updates/sec

Title: US-10-723-368-5
Perfect score: 254
Sequence: 1 TQAQLLRVGCVLGTCQVQNL.....MGPAGRQDSAPVDPSSPHSY 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	254	100.0	47	8	ADO61523	Ado61523 Human int
2	254	100.0	148	8	ADO61520	Ado61520 Human int
3	76	29.9	52	4	AAB91765	Aab91765 Adrenomed
4	72.5	28.5	52	4	AAB91759	Aab91759 Adrenomed
5	72.5	28.5	52	4	AAB75110	Aab75110 Human adr
6	72.5	28.5	52	4	AAE09818	Aae09818 Human adr
7	72.5	28.5	52	6	ABP55104	Abp55104 Human adr
8	72.5	28.5	52	7	ADC25152	Adc25152 Human ang
9	72.5	28.5	52	7	ADG91993	Adg91993 Human mat
10	72.5	28.5	52	8	ADM94034	Adm94034 Human AM
11	72.5	28.5	52	8	ADN03278	Adn03278 Exemplary
12	72.5	28.5	52	8	ADM98309	Adm98309 Mature hu
13	72.5	28.5	52	8	ADP18429	Adp18429 Neurogene
14	72.5	28.5	52	8	ADP18402	Adp18402 Neurogene
15	72.5	28.5	52	8	ADR42113	Adr42113 Adrenomed
16	72.5	28.5	53	4	AAB75111	Aab75111 Glycine e
17	72.5	28.5	53	4	AAB75112	Aab75112 Glycine e
18	72.5	28.5	53	6	ABJ18665	Abj18665 Universal
19	72.5	28.5	62	4	AAB75113	Aab75113 Linker pe
20	72.5	28.5	91	8	ADF55556	Adf55556 Active hu
21	72.5	28.5	120	4	AAB75123	Aab75123 UspA(1-56
22	72.5	28.5	120	4	AAB75122	Aab75122 UspA(1-57
23	72.5	28.5	120	6	ABJ18669	Abj18669 Universal
24	72.5	28.5	120	6	ABJ18670	Abj18670 Universal
25	72.5	28.5	147	4	AAB75124	Aab75124 UspA(1-84
26	72.5	28.5	147	6	ABJ18671	Abj18671 Universal
27	72.5	28.5	170	4	AAB75114	Aab75114 Thioredox
28	72.5	28.5	185	4	AAB60344	Aab60344 Human adr
29	72.5	28.5	185	4	AAB49697	Aab49697 Human adr
30	72.5	28.5	185	6	ABP72347	Abp72347 Adrenomed
31	72.5	28.5	185	7	ADA27595	Ada27595 Human adr
32	72.5	28.5	185	8	ADF55557	Adf55557 Human adr
33	72.5	28.5	185	8	ADN10849	Adn10849 Human adr
34	72.5	28.5	185	8	ADM98308	Adm98308 Human pre
35	72.5	28.5	185	8	ADP19855	Adp19855 Human pre
36	72.5	28.5	185	8	ADP12587	Adp12587 Protein e
37	72.5	28.5	185	8	ADO36937	Ado36937 Human pro
38	72.5	28.5	185	8	ADR14147	Adr14147 Human NF-
39	72.5	28.5	185	8	ADR87608	Adr87608 Human Adr
40	72.5	28.5	185	8	ADS19162	Ads19162 Human adr
41	72.5	28.5	186	7	ADD18582	Add18582 Human dis
42	72.5	28.5	206	6	ABJ18668	Abj18668 Universal
43	71.5	28.1	184	5	ABB57209	Abb57209 Mouse isc
44	71.5	28.1	184	8	ADO60040	Ado60040 CRH signa
45	70.5	27.8	188	4	AAB60345	Aab60345 Porcine a

ALIGNMENTS

RESULT 1
ADO61523
ID ADO61523 standard; protein; 47 AA.
XX
AC ADO61523;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human intermedin mature proetin SEQ ID NO:5.
XX
KW human; intermedin; hypotensive; gene therapy; hypertension;
KW cardioprotective; diet; prolactin release; growth hormone release;
KW ovarian follicle survival; oedema.
XX
OS Homo sapiens.
XX
PN WO2004048547-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US037968.
XX
PR 26-NOV-2002; 2002US-0429327P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Hsu SYT;
XX
DR WPI; 2004-441176/41.
XX
PT New composition comprises an intermedin peptide, useful for treating
PT hypertension, as cardioprotective agent, as a diet aid, for the release
PT of prolactin, or for growth hormone release from the pituitary.
XX
PS Disclosure; SEQ ID NO 5; 68pp; English.
XX
CC The invention relates to a novel composition comprising an intermedin
CC peptide, which comprises at least 18 contiguous amino acids in a sequence
CC comprising 148 amino acids (ADO61520). A composition of the invention has
CC hypotensive activity, and may have a use in gene therapy. The composition
CC comprising the intermedin peptide is useful for identifying homologous or
CC related genes, for production of the encoded peptide, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, for gene therapy, mapping functional regions of the protein, or
CC in studying associated physiological pathways. The intermedin peptide is
CC useful for treating hypertension, as a cardioprotective agent, as a diet
CC aid, for the release of prolactin, in growth hormone release from the
CC pituitary, or for ovarian follicle survival and growth. They are also

```
CC   useful in the reduction of oedema. The present sequence represents the
CC   human intermedin mature protein.
XX
SQ   Sequence 47 AA;

  Query Match             100.0%;  Score 254;  DB 8;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-27;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47


RESULT 2
ADO61520
ID   ADO61520 standard; protein; 148 AA.
XX
AC   ADO61520;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human intermedin SEQ ID NO:2.
XX
KW   human; intermedin; hypotensive; gene therapy; hypertension;
KW   cardioprotective; diet; prolactin release; growth hormone release;
KW   ovarian follicle survival; oedema.
XX
OS   Homo sapiens.
XX
PN   WO2004048547-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US037968.
XX
PR   26-NOV-2002; 2002US-0429327P.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Hsu SYT;
XX
DR   WPI; 2004-441176/41.
DR   N-PSDB; ADO61519.
XX
PT   New composition comprises an intermedin peptide, useful for treating
PT   hypertension, as cardioprotective agent, as a diet aid, for the release
PT   of prolactin, or for growth hormone release from the pituitary.
XX
PS   Claim 1; SEQ ID NO 2; 68pp; English.
XX
CC   The invention relates to a novel composition comprising an intermedin
CC   peptide, which comprises at least 18 contiguous amino acids in a sequence
CC   comprising 148 amino acids (ADO61520). A composition of the invention has
CC   hypotensive activity, and may have a use in gene therapy. The composition
CC   comprising the intermedin peptide is useful for identifying homologous or
CC   related genes, for production of the encoded peptide, in producing
CC   compositions that modulate the expression or function of its encoded
CC   protein, for gene therapy, mapping functional regions of the protein, or
CC   in studying associated physiological pathways. The intermedin peptide is
CC   useful for treating hypertension, as a cardioprotective agent, as a diet
CC   aid, for the release of prolactin, in growth hormone release from the
CC   pituitary, or for ovarian follicle survival and growth. They are also
CC   useful in the reduction of oedema. The present sequence represents the
CC   human intermedin protein of the invention.
XX
SQ   Sequence 148 AA;

  Query Match             100.0%;  Score 254;  DB 8;  Length 148;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-27;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 147


RESULT 3
AAB91765
ID   AAB91765 standard; peptide; 52 AA.
XX
AC   AAB91765;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Adrenomedullin peptide (AM) SEQ ID NO:941.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US013576.
XX
PR   17-MAY-1999;   99US-0134406P.
PR   10-SEP-1999;   99US-0153406P.
PR   15-OCT-1999;   99US-0159783P.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity.
XX
PS   Disclosure; Page 501; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity in
CC   vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention
XX
SQ   Sequence 52 AA;

  Query Match             29.9%;  Score 76;  DB 4;  Length 52;
  Best Local Similarity   35.9%;  Pred. No. 0.0091;
  Matches   14;  Conservative    6;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|     |    : :   ||  |
Db         14 GCRFGTCTVQKLAHQIYQFTDKDGVAPRSKISKISPQGY 52


RESULT 4
AAB91759
```

ID AAB91759 standard; peptide; 52 AA.
XX
AC AAB91759;
XX
DT 22-JUN-2001 (first entry)
XX
DE Adrenomedullin peptide (AM) SEQ ID NO:935.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 498; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 4; Length 52;
Best Local Similarity 38.5%; Pred. No. 0.028;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```
Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52
```

RESULT 5
AAB75110
ID AAB75110 standard; protein; 52 AA.
XX
AC AAB75110;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human adrenomedullin (AM) protein.
XX
KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS Homo sapiens.
XX
PN WO200127310-A1.
XX
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-JP007023.
XX
PR 15-OCT-1999; 99JP-00294147.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR WPI; 2001-282044/29.
DR N-PSDB; AAH19806.
XX
PT Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host.
XX
PS Disclosure; Page 45; 75pp; Japanese.
XX
CC The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and (c)
CC dissolving the sediment and extracting adrenomedullin precursor. The
CC method can be used for the production of adrenomedullin precursor for
CC pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and
CC AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention
XX
SQ Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 4; Length 52;
Best Local Similarity 38.5%; Pred. No. 0.028;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```
Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52
```

RESULT 6
AAE09818
ID AAE09818 standard; peptide; 52 AA.
XX
AC AAE09818;
XX
DT 29-NOV-2001 (first entry)
XX
DE Human adrenomedullin peptide #1.
XX
KW Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW CGRP-receptor identification; adrenomedullin.
XX
OS Homo sapiens.
XX
PN US6268474-B1.
XX
PD 31-JUL-2001.
XX
PF 30-APR-1998; 98US-00070504.
XX
PR 30-APR-1998; 98US-00070504.
XX
PA (UYCR-) UNIV CREIGHTON.

```
XX
PI   Smith DD,  Saha S,  Abel PW;
XX
DR   WPI; 2001-564216/63.
XX
PT   Vasoactive peptides useful for inhibiting calcitonin gene related peptide
PT   receptor activity.
XX
PS   Claim 5; Col 25-26; 24pp; English.
XX
CC   The invention relates to antagonists of the vasoactive peptide calcitonin
CC   gene related peptide (CGRP) and other members of the CGRP superfamily.
CC   The invention also relates to amino the terminal modifications of
CC   peptides to improve their ability to bind to a member of the CGRP-
CC   receptor super-family. CGRP antagonists are used for inhibiting CGRP
CC   activity which can be used in vitro e.g. in assays to identify and/or
CC   isolate CGRP receptors or with intact cells either in vitro or in vivo to
CC   inhibit the effect of CGRP binding to its receptor. The present sequence
CC   is human adrenomedullin peptide
XX
SQ   Sequence 52 AA;

  Query Match             28.5%;  Score 72.5;  DB 4;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.028;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 7
ABP55104
ID   ABP55104 standard; peptide; 52 AA.
XX
AC   ABP55104;
XX
DT   07-FEB-2003  (first entry)
XX
DE   Human adrenomedullin.
XX
KW   Adrenomedullin; human; protein engineering; solubility; aggregation;
KW   hypotensive; vasodilator; cyclic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  16. .21
XX
PN   WO200283734-A2.
XX
PD   24-OCT-2002.
XX
PF   17-APR-2002; 2002WO-GB001778.
XX
PR   17-APR-2001; 2001GB-00009438.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Zurdo J,  Dobson CM;
XX
DR   WPI; 2003-046916/04.
XX
PT   New modified human calcitonin peptide having reduced aggregation, useful
PT   for the treatment of Paget's disease, hypercalcemia and/or osteoporosis.
XX
PS   Example; Page 21; 35pp; English.
XX
CC   The present sequence is that of human adrenomedullin, a potent
CC   hypotensive and vasodilator. The invention provides modified calcitonin
CC   and related peptides, such as adrenomedullin, that have at least 70%
CC   identity to the native form but are modified such that the tendency of
CC   the peptide to aggregate is reduced. Preferred regions for modification
CC   include those for which the peptide is polymorphic amongst different
CC   species, which increase the propensity of the peptide to form local
CC   interactions of the alpha-helical type, or which reduce the number of
CC   hydrophobic residues or increase the net charge of the peptide. When
CC   aggregation is reduced or prevented, lower doses of the drug can be used.
CC   Side-effects and undesired responses are minimised by retaining high
CC   sequence identity to the human peptide
XX
SQ   Sequence 52 AA;

  Query Match             28.5%;  Score 72.5;  DB 6;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.028;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 8
ADC25152
ID   ADC25152 standard; peptide; 52 AA.
XX
AC   ADC25152;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human angiogenesis inhibiting peptide #SEQ ID 1.
XX
KW   Cytostatic; gene therapy; cancer; stomach; colon; pulmonary; ovarian;
KW   liver; pancreatic; human.
XX
OS   Homo sapiens.
XX
PN   WO2003078460-A1.
XX
PD   25-SEP-2003.
XX
PF   19-MAR-2003; 2003WO-JP003344.
XX
PR   19-MAR-2002; 2002JP-00075575.
XX
PA   (HOKK-) HOKKAIDO TECHNOLOGY LICENSING OFFICE CO.
XX
PI   Kobayashi M;
XX
DR   WPI; 2003-767505/72.
XX
PT   Peptides with effect on inhibiting angiogenesis in cancer cells and
PT   inhibiting proliferation of cancer cells, and encoded polynucleotides,
PT   applicable in drug compositions for treating cancer.
XX
PS   Claim 1; SEQ ID NO 1; 41pp; Japanese.
XX
CC   The invention relates to peptides comprising an amino acid sequence
CC   derived from a fully defined 52 amino acid sequence (S1) given in the
CC   specification. Peptides may be created by deletion of some amino acids
CC   from the N-terminal of S1. The peptides are applicable in drug
CC   compositions for treating cancer e.g. stomach cancer, colon cancer,
CC   pulmonary cancer, ovarian cancer, liver cancer or pancreatic cancer. The
CC   current sequence represents an angiogenesis inhibiting peptide of the
CC   invention.
XX
SQ   Sequence 52 AA;

  Query Match             28.5%;  Score 72.5;  DB 7;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.028;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52
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RESULT 9
ADG91993
ID   ADG91993 standard; protein; 52 AA.
XX
AC   ADG91993;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human mature adrenomedullin protein.
XX
KW   neuroleptic; antisense therapy; gene therapy; adrenomedullin agonist;
KW   schizophrenia; gene expression; decidual protein induced by progesterone;
KW   DEPP; adrenomedullin; cold shock domain protein A; csdA; antisense;
KW   siRNA; ribozyme; triple helix formation.
XX
OS   Homo sapiens.
XX
PN   WO2003078658-A2.
XX
PD   25-SEP-2003.
XX
PF   19-MAR-2003; 2003WO-EP002875.
XX
PR   20-MAR-2002; 2002US-0366001P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
XX
PI   Buxton FP,  Carpenter WT,  Roberts RC,  Tamminga CA;
XX
DR   WPI; 2003-767532/72.
XX
PT   Screening for schizophrenia in a population utilizing genes encoding the
PT   decidual protein induced by progesterone, adrenomedullin and/or cold
PT   shock domain protein A, useful in diagnosing, preventing and/or treating
PT   schizophrenia.
XX
PS   Disclosure; SEQ ID NO 1; 41pp; English.
XX
CC   The invention relates to a method of screening for schizophrenia in a
CC   population comprises determining the magnitude of expression, in members
CC   of the population, of at least one gene selected from the gene encoding
CC   decidual protein induced by progesterone (DEPP), the gene encoding
CC   adrenomedullin and the gene encoding cold shock domain protein A (csdA)
CC   in a sample, and comparing the magnitude of expression to a baseline of
CC   expression of the gene, where increased gene expression indicates the
CC   presence of schizophrenia. An antisense molecule, siRNA, ribozyme or
CC   nucleic acid molecule promoting triple helix formation that specifically
CC   inhibit the expression of DEPP, csdA or adrenomedullin genes, is useful
CC   for the manufacture of a medicament for the treatment of schizophrenia.
CC   An antibody that specifically binds an epitope of DEPP, csdA or
CC   adrenomedullin is also useful for the manufacture of a medicament for the
CC   treatment of schizophrenia. This sequence represents the mature
CC   adrenomedullin protein.
XX
SQ   Sequence 52 AA;

  Query Match             28.5%;  Score 72.5;  DB 7;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.028;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels .  1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 10
ADM94034
ID   ADM94034 standard; peptide; 52 AA.
XX
AC   ADM94034;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human AM peptide, a CRSP homologue.
XX
KW   calcitonin receptor stimulating peptide; CRSP; cAMP activity;
KW   skeletal disorder; cancer; hypertension; restenosis; analgesic;
KW   appetite suppressant; diuretic; vasotropic; cytostatic; diuretic;
KW   osteopathic; anorectic; hypotensive; human; AM.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  16. .21
FT   Modified-site   52
FT                   /note= "C-terminal amide"
XX
PN   WO2003102180-A1.
XX
PD   11-DEC-2003.
XX
PF   28-MAY-2003; 2003WO-JP006641.
XX
PR   04-JUN-2002; 2002JP-00162797.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA   (NINA-) JAPAN NAT CARDIOVASCULAR.
XX
PI   Minamino N,  Katafuchi T;
XX
DR   WPI; 2004-043113/04.
XX
PT   Calcitonin receptor stimulating peptides promoting cAMP production in
PT   cells for treatment of cancer, skeletal disorders and hypertension and as
PT   appetite suppressants and analgesics.
XX
PS   Disclosure; Fig 2; 62pp; Japanese.
XX
CC   This invention relates to novel calcitonin receptor stimulating peptides
CC   (CRSPs) that are expressed in the central nervous system and act on the
CC   calcitonin receptor to promote the production of cAMP within a cell.
CC   Specifically, it refers to CRSPs that can stimulate concentration
CC   dependent sodium ion uptake and furthermore act to inhibit calcium ion
CC   uptake by the cell. The present invention describes mutant peptides
CC   derived from the CRSPs that have additions, deletions and/ or
CC   substitutions of one or more amino acids, yet that retain similar
CC   activity and are useful for developing drug compositions and
CC   pharmaceutically acceptable carriers to treat and/ or prevent skeletal
CC   disorders, cancer, hypertension and restenosis. Furthermore, CRSPs can
CC   also be used as analgesics, appetite suppressants and diuretics such that
CC   exhibit vasotropic, cytostatic, diuretic, osteopathic, anorectic and
CC   hypotensive activities. This peptide sequence is a human AM peptide that
CC   has cAMP activity, given in an exemplification of the invention.
XX
SQ   Sequence 52 AA;

  Query Match             28.5%;  Score 72.5;  DB 8;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.028;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 11
ADN03278
ID   ADN03278 standard; peptide; 52 AA.
XX
AC   ADN03278;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Exemplary peptide ligand for proteome analysis  #2.
```

XX
KW Peptide ligand; proteome; capture compound; mass spectrometry;
KW protein separation;
KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.
XX
OS Unidentified.
XX
PN US2003119021-A1.
XX
PD 26-JUN-2003.
XX
PF 16-JUL-2002; 2002US-00197954.
XX
PR 16-JUL-2001; 2001US-0306019P.
PR 21-AUG-2001; 2001US-0314123P.
PR 11-MAR-2002; 2002US-0363433P.
XX
PA (KOST/) KOSTER H.
PA (SIDD/) SIDDIQI S.
PA (LITT/) LITTLE D P.
XX
PI Koster H, Siddiqi S, Little DP;
XX
DR WPI; 2004-059185/06.
XX
PT Collection of capture compounds capable of binding to biomolecules to
PT form complexes that are stable under mass spectrometry conditions, useful
PT for analysis of biomolecules, especially proteins.
XX
PS Disclosure; SEQ ID NO 2; 165pp; English.
XX
CC The invention relates to a collection of capture compounds capable of
CC binding to biomolecules to form complexes that are stable under mass
CC spectrometry conditions. The formulae for the capture compounds comprises
CC sets of compounds of formula (I)-(III) given in the specification. Also
CC included are analysis of biomolecules (by contacting a composition
CC comprising a biomolecule with the above collection and identifying or
CC detecting bound biomolecules), separating protein conformers (by
CC contacting a composition comprising a biomolecule with the above
CC collection, separating the members of the collection and identifying
CC bound proteins), reducing diversity of a complex mixture of biomolecules
CC (by contacting the mixture with the above collection and separating each
CC set of complexes of capture compounds with biomolecules from the other
CC sets) and identifying phenotype-specific biomolecules (by sorting cells
CC from a single subject into sets according to a phenotype, contacting
CC mixtures of biomolecules from each set with the above collection and
CC comparing the patterns of biomolecule binding from each set). The
CC collection of capture compounds is useful for the analysis of
CC biomolecules, especially proteins (e.g. analysis of a proteome), using
CC mass spectrometry, especially matrix assisted laser desorption ionisation
CC -time of flight (MALDI-TOF) mass spectrometry. The present sequence is an
CC exemplary peptide ligand which may be incorporated into a capture
CC compound of the invention.
XX
SQ Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 8; Length 52;
Best Local Similarity 38.5%; Pred. No. 0.028;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
|| ||| || |:|:::| : : || || |
Db 15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52

RESULT 12
ADM98309
ID ADM98309 standard; protein; 52 AA.
XX
AC ADM98309;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mature human adrenomedullin protein SeqID 3.
XX
KW AM(11-22); vasoconstriction; human; adrenomedullin; AM; vasoregulatory;
KW blood pressure; vasodilator; vasodilatory shock; septic shock;
KW haemorrhagic shock; vasotropic; hypotensive; immunosuppressive;
KW antibacterial.
XX
OS Homo sapiens.
XX
PN WO2004032708-A2.
XX
PD 22-APR-2004.
XX
PF 03-OCT-2003; 2003WO-US031400.
XX
PR 04-OCT-2002; 2002US-0416291P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Cuttitta F, Martinez A, Stetler-Stevenson WG, Unsworth EJ;
PI Saavedra JM;
XX
DR WPI; 2004-340778/31.
XX
PT New AM(11-22) peptides, useful for useful for inducing vasoconstriction,
PT for treating septic shock, vasodilatory shock or hemorrhagic shock, or
PT for reducing blood pressure.
XX
PS Disclosure; SEQ ID NO 3; 40pp; English.
XX
CC This invention relates to a novel peptide AM(11-22) useful for treating
CC shock, or in a pharmaceutical composition for inducing vasoconstriction.
CC Specifically, AM(11-22) is a short peptide derived from human
CC adrenomedullin (AM), which is a vasoregulatory compound that influences
CC blood pressure. The present invention describes screening assays to
CC identify compounds including antibodies, small molecule inhibitors or
CC peptides that modulate AM(11-22)-mediated vasoconstriction and as such
CC represent novel vasodilators or vasoconstrictors. Accordingly, AM(11-22)
CC can be used therapeutically in a pharmaceutical composition to inhibit
CC blood flow following traumatic or surgical injury, as well as for
CC vasodilatory, septic or haemorrhagic shock, and thus exhibits vasotropic,
CC hypotensive, immunosuppressive and antibacterial activities. This
CC polypeptide sequence is the mature human adrenomedullin protein of the
CC invention.
XX
SQ Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 8; Length 52;
Best Local Similarity 38.5%; Pred. No. 0.028;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
|| ||| || |:|:::| : : || || |
Db 15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52

RESULT 13
ADP18429
ID ADP18429 standard; protein; 52 AA.
XX
AC ADP18429;
XX
DT 26-AUG-2004 (first entry)
XX
DE Neurogenesis modulation-related protein SeqID43.
XX
KW neurogenesis modulation; neural tissue; central nervous system disorder;
KW neurodegenerative; ischaemic; learning and memory disorder;
KW neurological trauma; nootropic; neuroprotective; CNS-Gen;
KW cerebroprotective; vasotropic; anticonvulsant; antiparkinsonian;
KW haemostatic; hypertensive; muscular-Gen; ophthalmological;
KW antiinflammatory; analgesic; antidiabetic; neurogenesis modulator;
KW neural stem cell; progenitor cell;

KW neural tissue G-protein coupled receptor activator; neurogenesis inducer;
KW intracellular neural cAMP enhancer; intracellular neural cAMP stimulator;
KW intracellular neural Ca 2+ enhancer; Parkinson's disease;
KW Parkinson's disorder; Huntington's disease; Alzheimer's disease;
KW multiple sclerosis; amyotrophic lateral sclerosis; Shy-Drager syndrome;
KW progressive supranuclear palsy; Lewy body disease; spinal ischaemia;
KW ischaemic stroke; cerebral infarction; spinal cord injury;
KW cancer-related brain; spinal cord injury; multi-infarct dementia;
KW geriatric dementia; cAMP level; embryonic tissue; human.
XX
OS Homo sapiens.
XX
PN WO2004045592-A2.
XX
PD 03-JUN-2004.
XX
PF 20-NOV-2003; 2003WO-IB005311.
XX
PR 20-NOV-2002; 2002US-0427912P.
XX
PA (NEUR-) NEURONOVA AB.
PA (BERT/) BERTILSSON G.
PA (ERLA/) ERLANDSSON R.
PA (FRIS/) FRISEN J.
PA (HAEG/) HAEGESTRAND A.
PA (HEID/) HEIDRICH J.
PA (HELL/) HELLSTROEM K.
PA (HAEG/) HAEGGBLAD J.
PA (JANS/) JANSSON K.
PA (KORT/) KORTESMAA J.
PA (LIND/) LINDQUIST P.
PA (LUND/) LUNDH H.
PA (MCGU/) MCGUIRE J.
PA (MERC/) MERCER A.
PA (NJBE/) NJBERG K.
PA (OSSO/) OSSOINAK A.
PA (PATR/) PATRONE C.
PA (ROEN/) ROENNHOLM H.
PA (ZACH/) ZACHRISSON O.
PA (WIKS/) WIKSTROEM L.
XX
PI Bertilsson G, Erlandsson R, Frisen J, Haegestrand A, Heidrich J;
PI Hellstroem K, Haeggblad J, Jansson K, Kortesmaa J, Lindquist P;
PI Lundh H, Mcguire J, Mercer A, Njberg K, Ossoinak A, Patrone C;
PI Roennholm H, Zachrisson O, Wikstroem L;
XX
DR WPI; 2004-449666/42.
XX
PT Use of agent(s) that elevate intracellular cyclic adenosine monophosphate
PT or intracellular calcium levels in neural tissue for modulating
PT neurogenesis to treat central nervous system disorder.
XX
PS Disclosure; SEQ ID NO 43; 77pp; English.
XX
CC This invention relates to a novel method of modulating neurogenesis in
CC the neural tissue of a patient exhibiting symptom(s) of a central nervous
CC system disorder, such as neurodegenerative, ischaemic or learning and
CC memory disorder or neurological trauma. The method involves at least one
CC agent (A) that elevates intracellular cyclic adenosine monophosphate
CC (cAMP) levels or at least one agent (B) that elevates intracellular Ca 2+
CC levels in the neural tissue, which is administered where (A) modulates
CC and (B) induces neurogenesis. The invention may be useful for the
CC production of compounds with a nootropic, neuroprotective, CNS-Gen,
CC cerebroprotective, vasotropic, anticonvulsant, antiparkinsonian.
CC haemostatic, hypertensive, muscular-Gen, ophthalmological,
CC antiinflammatory, analgesic or antidiabetic activity. These compounds may
CC act as neurogenesis modulators, neural stem or progenitor cell
CC proliferation, differentiation and/or migration modulators, neural tissue
CC G-protein coupled receptor activators, neurogenesis inducers,
CC intracellular neural cAMP enhancers, intracellular neural cAMP
CC stimulators or intracellular neural Ca 2+ enhancers. The invention is
CC useful for modulating neurogenesis in neural tissue of a patient
CC exhibiting at least one symptom of central nervous system disorder, such
CC as Parkinson's disease and Parkinson's disorders, Huntington's disease,
CC Alzheimer's disease, multiple sclerosis, amyotrophic lateral sclerosis,
CC Shy-Drager syndrome, progressive supranuclear palsy, Lewy body disease,
CC spinal ischaemia, ischaemic stroke, cerebral infarction, spinal cord
CC injury, cancer-related brain and spinal cord injury, multi-infarct
CC dementia and geriatric dementia; for increasing the intracellular levels
CC of or stimulating cAMP levels in a cell (preferably a cell from a neural
CC tissue); and for in vitro modulation of neurogenesis. The agent modulates
CC neurogenesis in neural tissue by modulating proliferation,
CC differentiation, migration or survival of neural stem cells or progenitor
CC cells in the tissue; by maintaining or increasing the amount or
CC percentage of doublecortin positive cells in the neural tissue relative
CC to a patient not dosed with the agent or by activation of a G-protein
CC coupled receptor in the neural tissue. The method results in elevation of
CC cAMP levels of the neural stem cells by over 20% compared to untreated
CC tissue. The in vivo induction of neurogenesis allows treatment of
CC disorders caused by cell loss, injury or disease by endogenous
CC replacement and obviates the need for transplanting foreign cells into a
CC patient. Neurogenesis can also be induced by administration of the
CC neurogenesis-modulating agent directly into a desired site, which avoids
CC unnecessary systemic administration and possible side effects and further
CC provides an alternative to the use of drugs and the controversial use of
CC large quantities of embryonic tissue for treatment of Parkinson's
CC disease. The present sequence is that of a polypeptide which has been
CC shown to have the ability to increase intracellular cAMP levels and which
CC is related to the method of the invention.
XX
SQ Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 8; Length 52;
Best Local Similarity 38.5%; Pred. No. 0.028;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
|| ||| || |:|:::| : : || || |
Db 15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52

RESULT 14
ADP18402
ID ADP18402 standard; protein; 52 AA.
XX
AC ADP18402;
XX
DT 26-AUG-2004 (first entry)
XX
DE Neurogenesis modulation-related protein SeqID16.
XX
KW neurogenesis modulation; neural tissue; central nervous system disorder;
KW neurodegenerative; ischaemic; learning and memory disorder;
KW neurological trauma; nootropic; neuroprotective; CNS-Gen;
KW cerebroprotective; vasotropic; anticonvulsant; antiparkinsonian;
KW haemostatic; hypertensive; muscular-Gen; ophthalmological;
KW antiinflammatory; analgesic; antidiabetic; neurogenesis modulator;
KW neural stem cell; progenitor cell;
KW neural tissue G-protein coupled receptor activator; neurogenesis inducer;
KW intracellular neural cAMP enhancer; intracellular neural cAMP stimulator;
KW intracellular neural Ca 2+ enhancer; Parkinson's disease;
KW Parkinson's disorder; Huntington's disease; Alzheimer's disease;
KW multiple sclerosis; amyotrophic lateral sclerosis; Shy-Drager syndrome;
KW progressive supranuclear palsy; Lewy body disease; spinal ischaemia;
KW ischaemic stroke; cerebral infarction; spinal cord injury;
KW cancer-related brain; spinal cord injury; multi-infarct dementia;
KW geriatric dementia; cAMP level; embryonic tissue; human.
XX
OS Homo sapiens.
XX
PN WO2004045592-A2.
XX
PD 03-JUN-2004.
XX
PF 20-NOV-2003; 2003WO-IB005311.
XX

PR 20-NOV-2002; 2002US-0427912P.
XX
PA (NEUR-) NEURONOVA AB.
PA (BERT/) BERTILSSON G.
PA (ERLA/) ERLANDSSON R.
PA (FRIS/) FRISEN J.
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PA (HEID/) HEIDRICH J.
PA (HELL/) HELLSTROEM K.
PA (HAEG/) HAEGGBLAD J.
PA (JANS/) JANSSON K.
PA (KORT/) KORTESMAA J.
PA (LIND/) LINDQUIST P.
PA (LUND/) LUNDH H.
PA (MCGU/) MCGUIRE J.
PA (MERC/) MERCER A.
PA (NJBE/) NJBERG K.
PA (OSSO/) OSSOINAK A.
PA (PATR/) PATRONE C.
PA (ROEN/) ROENNHOLM H.
PA (ZACH/) ZACHRISSON O.
PA (WIKS/) WIKSTROEM L.
XX
PI Bertilsson G, Erlandsson R, Frisen J, Haegestrand A, Heidrich J;
PI Hellstroem K, Haeggblad J, Jansson K, Kortesmaa J, Lindquist P;
PI Lundh H, Mcguire J, Mercer A, Njberg K, Ossoinak A, Patrone C;
PI Roennholm H, Zachrisson O, Wikstroem L;
XX
DR WPI; 2004-449666/42.
XX
PT Use of agent(s) that elevate intracellular cyclic adenosine monophosphate
PT or intracellular calcium levels in neural tissue for modulating
PT neurogenesis to treat central nervous system disorder.
XX
PS Disclosure; SEQ ID NO 16; 77pp; English.
XX
CC This invention relates to a novel method of modulating neurogenesis in
CC the neural tissue of a patient exhibiting symptom(s) of a central nervous
CC system disorder, such as neurodegenerative, ischaemic or learning and
CC memory disorder or neurological trauma. The method involves at least one
CC agent (A) that elevates intracellular cyclic adenosine monophosphate
CC (cAMP) levels or at least one agent (B) that elevates intracellular Ca 2+
CC levels in the neural tissue, which is administered where (A) modulates
CC and (B) induces neurogenesis. The invention may be useful for the
CC production of compounds with a nootropic, neuroprotective, CNS-Gen,
CC cerebroprotective, vasotropic, anticonvulsant, antiparkinsonian.
CC haemostatic, hypertensive, muscular-Gen, ophthalmological,
CC antiinflammatory, analgesic or antidiabetic activity. These compounds may
CC act as neurogenesis modulators, neural stem or progenitor cell
CC proliferation, differentiation and/or migration modulators, neural tissue
CC G-protein coupled receptor activators, neurogenesis inducers,
CC intracellular neural cAMP enhancers, intracellular neural cAMP
CC stimulators or intracellular neural Ca 2+ enhancers. The invention is
CC useful for modulating neurogenesis in neural tissue of a patient
CC exhibiting at least one symptom of central nervous system disorder, such
CC as Parkinson's disease and Parkinson's disorders, Huntington's disease,
CC Alzheimer's disease, multiple sclerosis, amyotrophic lateral sclerosis,
CC Shy-Drager syndrome, progressive supranuclear palsy, Lewy body disease,
CC spinal ischaemia, ischaemic stroke, cerebral infarction, spinal cord
CC injury, cancer-related brain and spinal cord injury, multi-infarct
CC dementia and geriatric dementia; for increasing the intracellular levels
CC of or stimulating cAMP levels in a cell (preferably a cell from a neural
CC tissue); and for in vitro modulation of neurogenesis. The agent modulates
CC neurogenesis in neural tissue by modulating proliferation,
CC differentiation, migration or survival of neural stem cells or progenitor
CC cells in the tissue; by maintaining or increasing the amount or
CC percentage of doublecortin positive cells in the neural tissue relative
CC to a patient not dosed with the agent or by activation of a G-protein
CC coupled receptor in the neural tissue. The method results in elevation of
CC cAMP levels of the neural stem cells by over 20% compared to untreated
CC tissue. The in vivo induction of neurogenesis allows treatment of
CC disorders caused by cell loss, injury or disease by endogenous
CC replacement and obviates the need for transplanting foreign cells into a
CC patient. Neurogenesis can also be induced by administration of the
CC neurogenesis-modulating agent directly into a desired site, which avoids
CC unnecessary systemic administration and possible side effects and further
CC provides an alternative to the use of drugs and the controversial use of
CC large quantities of embryonic tissue for treatment of Parkinson's
CC disease. The present sequence is that of a polypeptide which has been
CC shown to have the ability to increase intracellular cAMP levels and which
CC is related to the method of the invention.
XX
SQ Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 8; Length 52;
Best Local Similarity 38.5%; Pred. No. 0.028;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
|| ||| || |:|:::| : : || || |
Db 15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52

RESULT 15
ADR42113
ID ADR42113 standard; peptide; 52 AA.
XX
AC ADR42113;
XX
DT 21-OCT-2004 (first entry)
XX
DE Adrenomedullin related peptide ligand, SEQ ID 2.
XX
KW Human; ligand; Adrenomedullin.
XX
OS Homo sapiens.
XX
PN WO2004064972-A2.
XX
PD 05-AUG-2004.
XX
PF 16-JAN-2004; 2004WO-US001037.
XX
PR 16-JAN-2003; 2003US-0441398P.
XX
PA (HKPH-) HK PHARM INC.
PA (KOES/) KOESTER H.
XX
PI Koester H, Little DP, Siddiqi SM, Grealish MP, Marappan S;
PI Hassman CF, Yip P;
XX
DR WPI; 2004-642213/62.
XX
PT Identifying drug non-target biomolecules in mixture of biomolecules
PT involves interacting mixture of biomolecules with capture compounds
PT having high binding affinity and analyzing captured biomolecules to
PT identify drug non-targets.
XX
PS Disclosure; SEQ ID NO 2; 368pp; English.
XX
CC The present invention relates to a method for identifying drug non-target
CC biomolecules in a mixture of biomolecules. The method comprises
CC interacting mixture with capture compounds having moiety X which
CC covalently binds to biomolecules with high affinity, moiety Y that
CC increases selectivity of binding so that the capture compound binds to
CC fewer biomolecules, and moiety Z for presenting X and Y, and analysing
CC captured biomolecules to identify drug non-targets. The capture compound
CC also optionally comprises a sorting function moiety Q and or a solubility
CC function moiety W. The selectivity function moiety Y serves to modulate
CC the reactivity function by reducing the number of groups to which the
CC reactivity function moiety X bind, such as by steric hindrance and other
CC interactions. Y is optionally a peptide ligand (ADR42112-ADR42256).
XX
SQ Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 8; Length 52;

Best Local Similarity 38.5%; Pred. No. 0.028;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```
Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52
```

Search completed: May 4, 2005, 18:11:09
Job time : 164 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2005, 17:57:34 ; Search time 176 Seconds
(without alignments)
136.748 Million cell updates/sec

Title: US-10-723-368-5
Perfect score: 254
Sequence: 1 TQAQLLRVGCVLGTCQVQNL.....MGPAGRQDSAPVDPSSPHSY 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	254	100.0	148	1	ADM2_HUMAN	Q7z4h4 homo sapien
2	228	89.8	150	1	ADM2_MOUSE	Q7tnk8 mus musculu
3	225	88.6	146	1	ADM2_RAT	P61312 rattus norv
4	188	74.0	159	2	Q75XW6	Q75xw6 fugu rubrip
5	187	73.6	168	2	Q75XW7	Q75xw7 fugu rubrip
6	185.5	73.0	140	2	Q6IFS9	Q6ifs9 brachydanio
7	87.5	34.4	174	2	Q75XW8	Q75xw8 fugu rubrip
8	83	32.7	123	2	Q75XW4	Q75xw4 fugu rubrip
9	78.5	30.9	171	2	Q6L8K5	Q6l8k5 cyprinus ca
10	72.5	28.5	185	1	ADML_HUMAN	P35318 homo sapien
11	71.5	28.1	184	1	ADML_MOUSE	P97297 mus musculu
12	71.5	28.1	188	1	ADML_BOVIN	O62827 bos taurus
13	71.5	28.1	188	2	Q95KP0	Q95kp0 bos taurus
14	70.5	27.8	188	1	ADML_PIG	P53366 sus scrofa
15	70	27.6	927	2	Q7S575	Q7s575 neurospora
16	69.5	27.4	185	1	ADML_RAT	P43145 rattus norv
17	69.5	27.4	188	1	ADML_CANFA	O77559 canis famil
18	64	25.2	388	2	Q8DGJ0	Q8dgj0 synechococc
19	63	24.8	798	2	Q6BYR2	Q6byr2 debaryomyce
20	59	23.2	142	2	Q6P390	Q6p390 homo sapien
21	59	23.2	386	2	Q7ZXW1	Q7zxw1 xenopus lae
22	59	23.2	506	2	Q6D6B0	Q6d6b0 erwinia car
23	58.5	23.0	576	2	Q8N2F7	Q8n2f7 homo sapien
24	58.5	23.0	1281	2	Q6NRI9	Q6nri9 xenopus lae
25	58	22.8	281	2	Q93RX1	Q93rx1 streptomyce
26	58	22.8	339	2	Q8YGC6	Q8ygc6 brucella me
27	58	22.8	351	2	Q6TFC2	Q6tfc2 clostridium
28	58	22.8	516	2	Q9P775	Q9p775 schizosacch
29	58	22.8	551	2	Q769I2	Q769i2 ciona intes
30	58	22.8	557	2	Q8G1J5	Q8g1j5 brucella su
31	58	22.8	559	2	Q9QW71	Q9qw71 rattus sp.
32	58	22.8	1306	2	Q95QM6	Q95qm6 caenorhabdi
33	58	22.8	1544	2	Q19194	Q19194 caenorhabdi
34	58	22.8	1557	2	Q8WPK9	Q8wpk9 oikopleura
35	57	22.4	82	2	Q6ERM3	Q6erm3 oryza sativ
36	57	22.4	810	1	ZCC5_HUMAN	Q9c0b0 homo sapien
37	57	22.4	810	1	ZCC5_MOUSE	Q8bl48 mus musculu
38	57	22.4	810	2	Q6EE22	Q6ee22 canis famil
39	57	22.4	811	2	Q7ZWS6	Q7zws6 xenopus lae
40	57	22.4	1057	2	Q7Q1Z9	Q7q1z9 anopheles g
41	57	22.4	1784	2	Q94606	Q94606 leishmania
42	56.5	22.2	521	2	Q6INA0	Q6ina0 homo sapien
43	56	22.0	184	2	Q92N11	Q92n11 rhizobium m
44	55.5	21.9	411	2	Q99PY2	Q99py2 streptomyce
45	55.5	21.9	528	2	Q88R34	Q88r34 pseudomonas

ALIGNMENTS

RESULT 1
ADM2_HUMAN
ID ADM2_HUMAN STANDARD; PRT; 148 AA.
AC Q7Z4H4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
GN Name=ADM2; Synonyms=AM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=14615490; DOI=10.1074/jbc.M305332200;
RA Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.T.;
RT "Intermedin is a calcitonin/calcitonin gene-related peptide family
RT peptide acting through the calcitonin receptor-like receptor/receptor
RT activity-modifying protein receptor complexes.";
RL J. Biol. Chem. 279:7264-7274(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;
RA Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.;
RT "Identification of novel adrenomedullin in mammals: a potent
RT cardiovascular and renal regulator.";
RL FEBS Lett. 556:53-58(2004).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

```
RA   Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA   Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA   Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA   Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA   Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA   Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA   Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA   Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA   Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA   Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA   Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA   Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA   Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA   Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA   Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA   Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA   Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA   Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA   O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA   Khan A.S., Lane L., Tilahun Y., Wright H.;
RT   "The DNA sequence of human chromosome 22.";
RL   Nature 402:489-495(1999).
CC   -!- FUNCTION: IMDL and IMDS may play a role as physiological
CC       regulators of gastrointestinal, cardiovascular bioactivities
CC       mediated by the CALCRL/RAMPs receptor complexes. Activates the
CC       cAMP-dependent pathway.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in the esophagus, stomach, jejunum,
CC       ileum, ileocecum, ascending colon, transverse colon, descending
CC       colon and rectum.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF529213; AAQ09100.1; -.
DR   EMBL; AB121034; BAD07411.1; -.
DR   EMBL; AL096767; -; NOT_ANNOTATED_CDS.
DR   Genew; HGNC:28898; ADM2.
DR   MIM; 608682; -.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL       1     24       Potential.
FT   PROPEP       25    98       By similarity.
FT   PEPTIDE      101   147      Adrenomedullin 2 (By similarity).
FT   PEPTIDE      108   147      Intermedin-short (Potential).
FT   DISULFID     110   115      By similarity.
FT   MOD_RES      147   147      Tyrosine amide (G-148 provides amide
FT                               group) (Probable).
SQ   SEQUENCE   148 AA;  15865 MW;  6E0E3098CFCE5BF2 CRC64;

  Query Match             100.0%;  Score 254;  DB 1;  Length 148;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-24;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 147


RESULT 2
ADM2_MOUSE
ID   ADM2_MOUSE      STANDARD;      PRT;   150 AA.
AC   Q7TNK8;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE   (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
GN   Name=Adm2; Synonyms=Am2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   STRAIN=C57BL/6;
RX   PubMed=14615490; DOI=10.1074/jbc.M305332200;
RA   Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.T.;
RT   "Intermedin is a calcitonin/calcitonin gene-related peptide family
RT   peptide acting through the calcitonin receptor-like receptor/receptor
RT   activity-modifying protein receptor complexes.";
RL   J. Biol. Chem. 279:7264-7274(2004).
RN   [2]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Kidney;
RX   PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;
RA   Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.;
RT   "Identification of novel adrenomedullin in mammals: a potent
RT   cardiovascular and renal regulator.";
RL   FEBS Lett. 556:53-58(2004).
CC   -!- FUNCTION: IMDL and IMDS may play a role as physiological
CC       regulators of gastrointestinal, cardiovascular bioactivities
CC       mediated by the CALCRL/RAMPs receptor complexes. Activates the
CC       cAMP-dependent pathway.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: High expression detected in the submaxillary
CC       gland, kidney, stomach, and mesentery, followed by the pituitary,
CC       lung, pancreas, intestines, spleen, thymus and ovary. Expressed
CC       mainly in the intermediate lobe of the pituitary, with sporadic in
CC       the anterior lobe.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF529212; AAQ09099.1; -.
DR   EMBL; AB121035; BAD07412.1; -.
DR   MGD; MGI:2675256; Adm2.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL       1     25       Potential.
FT   PROPEP       26    100      By similarity.
FT   PEPTIDE      103   149      Adrenomedullin 2 (By similarity).
FT   PEPTIDE      110   149      Intermedin-short (Potential).
FT   DISULFID     112   117      By similarity.
FT   MOD_RES      149   149      Tyrosine amide (G-150 provides amide
FT                               group) (Probable).
SQ   SEQUENCE   150 AA;  16188 MW;  2BFF392BFBFDEBBA CRC64;

  Query Match             89.8%;  Score 228;  DB 1;  Length 150;
  Best Local Similarity   93.3%;  Pred. No. 2.6e-21;
  Matches   42;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 AQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              |||||||||||||||||||||||: ||||:||||||||||||||
Db        105 AQLLRVGCVLGTCQVQNLSHRLWQLVRPAGRRDSAPVDPSSPHSY 149


RESULT 3
ADM2_RAT
ID   ADM2_RAT        STANDARD;      PRT;   146 AA.
AC   P61312;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE   (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
```

```
GN   Name=Adm2; Synonyms=Am2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;
RA   Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.;
RT   "Identification of novel adrenomedullin in mammals: a potent
RT   cardiovascular and renal regulator.";
RL   FEBS Lett. 556:53-58(2004).
RN   [2]
RP   FUNCTION, AND TISSUE SPECIFICITY.
RX   PubMed=14615490; DOI=10.1074/jbc.M305332200;
RA   Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.T.;
RT   "Intermedin is a calcitonin/calcitonin gene-related peptide family
RT   peptide acting through the calcitonin receptor-like receptor/receptor
RT   activity-modifying protein receptor complexes.";
RL   J. Biol. Chem. 279:7264-7274(2004).
CC   -!- FUNCTION: IMDL and IMDS may play a role as physiological
CC       regulators of gastrointestinal, cardiovascular bioactivities
CC       mediated by the CALCRL/RAMPs receptor complexes. Activates the
CC       cAMP-dependent pathway.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expression was restricted to the intermediate
CC       and anterior lobes of the pituitary.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB121036; BAD07413.1; -.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL       1     25       Potential.
FT   PROPEP      26     96       By similarity.
FT   PEPTIDE      99    145       Adrenomedullin 2 (By similarity).
FT   PEPTIDE     106    145       Intermedin-short (Potential).
FT   DISULFID    108    113       By similarity.
FT   MOD_RES     145    145       Tyrosine amide (G-146 provides amide
FT                                group) (Probable).
SQ   SEQUENCE   146 AA;  15572 MW;  C87043237AD29DDC CRC64;

  Query Match             88.6%;  Score 225;  DB 1;  Length 146;
  Best Local Similarity   91.1%;  Pred. No. 6.2e-21;
  Matches   41;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 AQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              |||||||||||||||||||||||||: |:||:|||||||||||||
Db        101 AQLLRVGCVLGTCQVQNLSHRLWQLVRPSGRRDSAPVDPSSPHSY 145


RESULT 4
Q75XW6
ID   Q75XW6      PRELIMINARY;      PRT;   159 AA.
AC   Q75XW6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin-3.
GN   Name=ADM3;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22984567; PubMed=14623291; DOI=10.1016/j.bbrc.2003.10.111;
RA   Ogoshi M., Inoue K., Takei Y.;
RT   "Identification of a novel adrenomedullin gene family in teleost
RT   fish.";
RL   Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR   EMBL; AB120297; BAD02343.1; -.
SQ   SEQUENCE   159 AA;  18028 MW;  F1863B20100E254D CRC64;

  Query Match             74.0%;  Score 188;  DB 2;  Length 159;
  Best Local Similarity   72.7%;  Pred. No. 4e-16;
  Matches   32;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 QLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||:| || |||||||||||||:||:| :|| ||:|::| |||||
Db        115 QLIRAGCALGTCQVQNLSHRLYQLIGQSGRDDSSPINPKSPHSY 158


RESULT 5
Q75XW7
ID   Q75XW7      PRELIMINARY;      PRT;   168 AA.
AC   Q75XW7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin-2.
GN   Name=ADM2;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22984567; PubMed=14623291; DOI=10.1016/j.bbrc.2003.10.111;
RA   Ogoshi M., Inoue K., Takei Y.;
RT   "Identification of a novel adrenomedullin gene family in teleost
RT   fish.";
RL   Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR   EMBL; AB120296; BAD02342.1; -.
DR   InterPro; IPR001938; Thaumatin.
SQ   SEQUENCE   168 AA;  18544 MW;  A5905E7CC112669B CRC64;

  Query Match             73.6%;  Score 187;  DB 2;  Length 168;
  Best Local Similarity   68.1%;  Pred. No. 5.6e-16;
  Matches   32;  Conservative   10;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              : :||:|| |||||||||||||||:||:| :|::||:|::| |||||
Db        121 SHGQLMRVACVLGTCQVQNLSHRLYQLIGQSGKEDSSPMNPHSPHSY 167


RESULT 6
Q6IFS9
ID   Q6IFS9      PRELIMINARY;      PRT;   140 AA.
AC   Q6IFS9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Intermedin (Fragment).
GN   Name=IMDN;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14615490; DOI=10.1074/jbc.M305332200;
RA   Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.;
RT   "Intermedin is a calcitonin/CGRP family peptide acting through the
```

```
RT   CRLR/RAMP receptor complexes.";
RL   J. Biol. Chem. 0:0-0(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hsu S.Y.T.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
DR   EMBL; BK004089; DAA04555.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   140 AA;  15816 MW;  509F74908C0DC75D CRC64;

  Query Match             73.0%;  Score 185.5;  DB 2;  Length 140;
  Best Local Similarity   77.3%;  Pred. No. 7.2e-16;
  Matches   34;  Conservative    7;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          4 QLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||:|||||||||||||||||:||:| :||:|| |::| |||||
Db         97 QLMRVGCVLGTCQVQNLSHRLYQLVGQSGREDS-PINPRSPHSY 139


RESULT 7
Q75XW8
ID   Q75XW8      PRELIMINARY;      PRT;   174 AA.
AC   Q75XW8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin-1.
GN   Name=ADM1;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22984567; PubMed=14623291; DOI=10.1016/j.bbrc.2003.10.111;
RA   Ogoshi M., Inoue K., Takei Y.;
RT   "Identification of a novel adrenomedullin gene family in teleost
RT   fish.";
RL   Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR   EMBL; AB120295; BAD02341.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
SQ   SEQUENCE   174 AA;  20222 MW;  61535E41FCF88D4D CRC64;

  Query Match             34.4%;  Score 87.5;  DB 2;  Length 174;
  Best Local Similarity   53.8%;  Pred. No. 0.0038;
  Matches   21;  Conservative    3;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              || |||| | :|: || || |   : | ||||  ||  |
Db         95 GCSLGTCTVHDLAFRLHQL-GFQYKIDIAPVDKISPQGY 132


RESULT 8
Q75XW4
ID   Q75XW4      PRELIMINARY;      PRT;   123 AA.
AC   Q75XW4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin-5.
GN   Name=ADM5;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22984567; PubMed=14623291; DOI=10.1016/j.bbrc.2003.10.111;
RA   Ogoshi M., Inoue K., Takei Y.;
RT   "Identification of a novel adrenomedullin gene family in teleost
RT   fish.";
RL   Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR   EMBL; AB120299; BAD02345.1; -.
SQ   SEQUENCE   123 AA;  13538 MW;  D3ED4CDBCFC4ECEB CRC64;

  Query Match             32.7%;  Score 83;  DB 2;  Length 123;
  Best Local Similarity   41.0%;  Pred. No. 0.0098;
  Matches   16;  Conservative    9;  Mismatches   12;  Indels    2;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              || :||||| ||:::|:|:    |: :|  |  : |  |
Db         85 GCQVGTCQVHNLANKLYQIGQRQGKDESTKV--NDPQGY 121


RESULT 9
Q6L8K5
ID   Q6L8K5      PRELIMINARY;      PRT;   171 AA.
AC   Q6L8K5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Preproadrenomedullin precursor.
GN   Name=preproAM;
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   PubMed=15242754; DOI=10.1016/j.ygcen.2004.05.002;
RA   Kono T., Sakai M.;
RT   "Molecular cloning and expression of preproadrenomedullin gene from
RT   common carp Cyprinus carpio L.";
RL   Gen. Comp. Endocrinol. 138:78-88(2004).
DR   EMBL; AB120940; BAD19046.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001710; Adrenomedullin.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        79    127       adrenomedullin.
SQ   SEQUENCE   171 AA;  19412 MW;  A9595B9A11E5AC36 CRC64;

  Query Match             30.9%;  Score 78.5;  DB 2;  Length 171;
  Best Local Similarity   42.2%;  Pred. No. 0.053;
  Matches   19;  Conservative    5;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          3 AQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              :|  | || |||| |  |:|||  |      :  :|| |  :|  |
Db         84 SQSRRSGCSLGTCTVHVLAHRLHDLNNKL-KIGNAPADKINPFGY 127


RESULT 10
ADML_HUMAN
ID   ADML_HUMAN     STANDARD;      PRT;   185 AA.
AC   P35318;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM; Synonyms=AM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93343928; PubMed=7688224;
RA   Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT   "Cloning and characterization of cDNA encoding a precursor for human
RT   adrenomedullin.";
RL   Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94354869; PubMed=8074714;
RA   Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,
RA   Kitamura K., Eto T., Matsuo H.;
RT   "Genomic structure of human adrenomedullin gene.";
RL   Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 95-146.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93249425; PubMed=8387282;
RA   Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA   Matsuo H., Eto T.;
RT   "Adrenomedullin: a novel hypotensive peptide isolated from human
RT   pheochromocytoma.";
RL   Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN   [5]
RP   REVIEW.
RX   MEDLINE=98240137; PubMed=9578982; DOI=10.1006/frne.1998.0164;
RA   Samson W.K.;
RT   "Proadrenomedullin-derived peptides.";
RL   Front. Neuroendocrinol. 19:100-127(1998).
RN   [6]
RP   REVIEW.
RX   MEDLINE=20053666; PubMed=10588445; DOI=10.1016/S0167-0115(99)00025-7;
RA   Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
RT   "Structure-activity relationships of adrenomedullin in the circulation
RT   and adrenal gland.";
RL   Regul. Pept. 85:1-8(1999).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents. Numerous actions have been reported most related to the
CC       physiologic control of fluid and electrolyte homeostasis. In the
CC       kidney, am is diuretic and natriuretic, and both am and pamp
CC       inhibit aldosterone secretion by direct adrenal actions. In
CC       pituitary gland, both peptides at physiologically relevant doses
CC       inhibit basal ACTH secretion. Both peptides appear to act in brain
CC       and pituitary gland to facilitate the loss of plasma volume,
CC       actions which complement their hypotensive effects in blood
CC       vessels.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highest levels found in pheochromocytoma and
CC       adrenal medulla. Also found in lung, ventricle and kidney tissues.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D14874; BAA03589.1; -.
DR   EMBL; S73906; AAC60642.1; -.
DR   EMBL; BC015961; AAH15961.1; -.
DR   EMBL; D43639; BAA07756.1; ALT_SEQ.
DR   PIR; JC2351; JN0684.
DR   Genew; HGNC:259; ADM.
DR   H-InvDB; HIX0009441; -.
DR   MIM; 103275; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0006171; P:cAMP biosynthesis; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0008015; P:circulation; TAS.
DR   GO; GO:0007565; P:pregnancy; TAS.
DR   GO; GO:0006701; P:progesterone biosynthesis; TAS.
DR   GO; GO:0009611; P:response to wounding; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Polymorphism; Signal.
FT   SIGNAL       1     21
FT   PEPTIDE      22    41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45    92
FT   PEPTIDE      95    146      Adrenomedullin.
FT   PROPEP       148   185      PreproAM C-terminal fragment.
FT   DISULFID     110   115
FT   MOD_RES      41    41       Arginine amide (G-42 provides amide
FT                               group).
FT   MOD_RES      146   146      Tyrosine amide (G-147 provides amide
FT                               group).
FT   VARIANT      50    50       S -> R (in dbSNP:5005).
FT                               /FTId=VAR_014861.
SQ   SEQUENCE   185 AA;  20420 MW;  64C7D2A0B4654DFE CRC64;

  Query Match             28.5%;  Score 72.5;  DB 1;  Length 185;
  Best Local Similarity   38.5%;  Pred. No. 0.34;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146


RESULT 11
ADML_MOUSE
ID   ADML_MOUSE     STANDARD;      PRT;   184 AA.
AC   P97297; P97453;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=Adm;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=97092892; PubMed=8938454; DOI=10.1006/geno.1996.0576;
RA   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
RA   Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RT   "Genomic organization, expression, and chromosomal mapping of the
RT   mouse adrenomedullin gene.";
RL   Genomics 37:395-399(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=99046755; PubMed=9808778; DOI=10.1006/dbio.1998.9073;
RA   Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
RA   Ko M.S.H.;
RT   "Expression of adrenomedullin, a hypotensive peptide, in the
RT   trophoblast giant cells at the embryo implantation site in mouse.";
RL   Dev. Biol. 203:264-275(1998).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D78349; BAA11367.1; -.
DR   EMBL; U77630; AAB36535.1; -.
DR   MGD; MGI:108058; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL       1     21       By similarity.
FT   PEPTIDE      22    41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45    92       By similarity.
ET   PEPTIDE      95    144      Adrenomedullin.
FT   PROPEP      151    184      PreproAM C-terminal fragment (By
FT                               similarity).
FT   DISULFID    108    113      By similarity.
FT   MOD_RES      41     41      Arginine amide (G-42 provides amide
FT                               group) (By similarity).
FT   MOD_RES     144    144      Tyrosine amide (G-145 provides amide
FT                               group) (By similarity).
FT   CONFLICT    173    173      A -> G (in Ref. 2).
SQ   SEQUENCE   184 AA;  20764 MW;  C88C99045A79C898 CRC64;

  Query Match             28.1%;  Score 71.5;  DB 1;  Length 184;
  Best Local Similarity   38.5%;  Pred. No. 0.46;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  |||  | |:|:::||     :   || :  ||  |
Db        107 GCRFGTCTFQKLAHQIYQLT-DKDKDGMAPRNKISPQGY 144


RESULT 12
ADML_BOVIN
ID   ADML_BOVIN     STANDARD;      PRT;   188 AA.
AC   O62827;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98244567; PubMed=9585168; DOI=10.1016/S0024-3205(98)00079-4;
RA   Barker S., Wood E., Clark A.J.L., Corder R.;
RT   "Cloning of bovine preproadrenomedullin and inhibition of its basal
RT   expression in vascular endothelial cells by staurosporine.";
RL   Life Sci. 62:1407-1415(1998).
CC   -!- FUNCTION: Hypotensive peptide. May function as a hormone in
CC       circulation control (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001613; CAA04866.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL       1     21       By similarity.
FT   PEPTIDE      22    41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45    92       By similarity.
FT   PEPTIDE      95    146      Adrenomedullin.
FT   PROPEP      148    188      PreproAM C-terminal fragment (By
FT                               similarity).
FT   DISULFID    110    115      By similarity.
FT   MOD_RES      41     41      Arginine amide (G-42 provides amide
FT                               group) (By similarity).
FT   MOD_RES     146    146      Tyrosine amide (G-147 provides amide
FT                               group) (By similarity).
SQ   SEQUENCE   188 AA;  20981 MW;  3002E79AB3B6612C CRC64;

  Query Match             28.1%;  Score 71.5;  DB 1;  Length 188;
  Best Local Similarity   38.5%;  Pred. No. 0.47;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  |||  | |:|:::      :  |||    ||  |
Db        109 GCRFGTCTVQKLAHQIYHFT-DKDKDGSAPRSKISPQGY 146


RESULT 13
Q95KP0
ID   Q95KP0      PRELIMINARY;      PRT;   188 AA.
AC   Q95KP0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Adrenomedullin.
GN   Name=pBAM-2;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21630318; PubMed=11754956; DOI=10.1016/S0196-9781(01)00529-0;
RA   Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
RA   Kangawa K., Eto T.;
RT   "Adrenomedullin (11-26): a novel endogenous hypertensive peptide
RT   isolated from bovine adrenal medulla.";
RL   Peptides 22:1713-1718(2001).
DR   EMBL; AB055107; BAB62176.1; -.
```

```
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
SQ   SEQUENCE   188 AA;  20963 MW;  6102E69A756DCA86 CRC64;

  Query Match             28.1%;  Score 71.5;  DB 2;  Length 188;
  Best Local Similarity   38.5%;  Pred. No. 0.47;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::       :  |||    ||  |
Db        109 GCRFGTCTVQKLAHQIYHFT-DKDKDGSAPRSKISPQGY 146


RESULT 14
ADML_PIG
ID   ADML_PIG       STANDARD;      PRT;   188 AA.
AC   P53366;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM; Synonyms=AM;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94139945; PubMed=8043068; DOI=10.1016/0014-5793(94)80289-0;
RA   Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
RT   "Complete amino acid sequence of porcine adrenomedullin and cloning of
RT   cDNA encoding its precursor.";
RL   FEBS Lett. 338:306-310(1994).
RN   [2]
RP   SEQUENCE OF 22-41.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94357274; PubMed=8076689; DOI=10.1016/0014-5793(94)00810-8;
RA   Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA   Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT   "Identification and hypotensive activity of proadrenomedullin N-
RT   terminal 20 peptide (PAMP).";
RL   FEBS Lett. 351:35-37(1994).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in adrenal glands, lung and
CC       kidney.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D14875; BAA03590.1; -.
DR   PIR; S41600; S41600.
DR   InterPro; IPR001710; Adrenomedullin.
DR   InterPro; IPR011038; Calycin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     21
FT   PEPTIDE       22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP        45     92
FT   PEPTIDE       95    146       Adrenomedullin.
FT   PROPEP       153    188       PreproAM C-terminal fragment (By
FT                                 similarity).
FT   DISULFID     110    115       By similarity.
FT   MOD_RES       41     41       Arginine amide (G-42 provides amide
FT                                 group).
FT   MOD_RES      146    146       Tyrosine amide (G-147 provides amide
FT                                 group).
SQ   SEQUENCE   188 AA;  20893 MW;  71749460F5660A61 CRC64;

  Query Match             27.8%;  Score 70.5;  DB 1;  Length 188;
  Best Local Similarity   38.5%;  Pred. No. 0.63;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|       :   ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDGVAPRSKISPQGY 146


RESULT 15
Q7S575
ID   Q7S575       PRELIMINARY;      PRT;   927 AA.
AC   Q7S575;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=NCU02295.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000355; EAA30703.1; -.
DR   HSSP; P78356; 1BO1.
DR   GO; GO:0016308; F:1-phosphatidylinositol-4-phosphate 5-kinase. . .; IEA.
DR   InterPro; IPR002498; PIP5K.
DR   Pfam; PF01504; PIP5K; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   927 AA;  102558 MW;  21FDC49FA419E932 CRC64;

  Query Match             27.6%;  Score 70;  DB 2;  Length 927;
  Best Local Similarity   72.2%;  Pred. No. 4.2;
  Matches   13;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         30 PAGRQDSAPVDPSSPHSY 47
              || |:|||  ||||| |
Db        123 PAQRRDSAPSSPSSPHRY 140


Search completed: May  4, 2005, 18:14:12
Job time : 178 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2005, 17:58:05 ; Search time 39 Seconds
(without alignments)
115.954 Million cell updates/sec

Title: US-10-723-368-5
Perfect score: 254
Sequence: 1 TQAQLLRVGCVLGTCQVQNL.....MGPAGRQDSAPVDPSSPHSY 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	72.5	28.5	185	2	JN0684	adrenomedullin pre
2	70.5	27.8	188	2	S41600	adrenomedullin - p
3	69.5	27.4	185	2	JN0766	adrenomedullin pre
4	58	22.8	339	2	AC3406	l-lactate permease
5	58	22.8	560	2	A38731	alpha-1A adrenergi
6	58	22.8	1544	2	T29482	hypothetical prote
7	57	22.4	1784	2	T02844	cdc16-related prot
8	54	21.3	283	2	E82662	ABC transporter AT
9	54	21.3	792	2	T26050	hypothetical prote
10	53.5	21.1	303	2	A43708	gamma-interferon-i
11	53.5	21.1	345	2	A37845	carboxylesterase (
12	53	20.9	136	2	T35335	hypothetical prote
13	53	20.9	192	2	AE2414	hypothetical prote
14	53	20.9	272	2	H95954	probable Sir2-like
15	53	20.9	351	2	E97187	dTDP-D-glucose 4,6
16	53	20.9	450	2	S07051	cysteine proteinas
17	53	20.9	450	2	S12099	cysteine proteinas
18	53	20.9	765	2	S74598	hypothetical prote
19	53	20.9	860	2	JC5702	ErbB kinase activa
20	53	20.9	868	2	JC5701	ErbB kinase activa
21	52.5	20.7	347	2	T26349	hypothetical prote
22	52.5	20.7	910	2	AE3380	valine-tRNA ligase
23	52	20.5	381	2	S38663	hypothetical prote
24	52	20.5	665	2	C81439	probable integral
25	52	20.5	2870	2	H96974	cyclic beta 1-2 gl
26	52	20.5	3898	1	GNWVHB	genome polyprotein
27	52	20.5	3898	2	S57437	genome polyprotein
28	52	20.5	3898	2	S58295	polyprotein - hog
29	51.5	20.3	461	2	B95388	Probable (EC 1.1.1
30	51.5	20.3	977	2	I52657	seizure-related pr
31	51	20.1	106	2	A05148	hypothetical reduc
32	51	20.1	407	2	I52703	42K membrane glyco
33	51	20.1	552	2	S15555	NAD synthase (EC 6
34	51	20.1	771	2	G71409	probable replicati
35	51	20.1	813	2	E85135	hypothetical prote
36	51	20.1	1359	2	T10235	xanthine dehydroge
37	51	20.1	3898	1	GNWVHC	genome polyprotein
38	51	20.1	4544	1	S02392	alpha-2-macroglobu
39	50.5	19.9	296	2	T12469	hypothetical prote
40	50.5	19.9	317	2	S22087	peroxidase (EC 1.1
41	50.5	19.9	397	2	T19022	hypothetical prote
42	50.5	19.9	460	2	AG2262	hypothetical prote
43	50.5	19.9	488	2	T31622	hypothetical prote
44	50.5	19.9	503	2	A85900	hypothetical prote
45	50.5	19.9	503	2	E91055	hypothetical prote

ALIGNMENTS

RESULT 1
JN0684
adrenomedullin precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC2351; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, T.;
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A;Title: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:94354869; PMID:8074714
A;Accession: JC2351
A;Molecule type: DNA
A;Residues: 1-185 <ISH>
A;Cross-references: UNIPROT:P35318; GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A;Experimental source: pheochromocytoma
R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A;Title: Cloning and characterization of cDNA encoding a precursor for human adrenomedul
A;Reference number: JN0684; MUID:93343928; PMID:7688224
A;Accession: JN0684
A;Molecule type: mRNA
A;Residues: 1-185 <KIT>
A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A;Accession: PN0548
A;Molecule type: protein
A;Residues: 22-41 <KI2>
R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A;Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocytoma
A;Reference number: JN0476; MUID:93249425; PMID:8387282
A;Accession: JN0476
A;Molecule type: protein
A;Residues: 95-146 <KI3>
A;Experimental source: pheochromocytoma
C;Genetics:
A;Gene: GDB:ADM
A;Cross-references: GDB:217070; OMIM:103275
A;Map position: 11pter-11qter
A;Introns: 33/2; 83/2
C;Keywords: amidated carboxyl end; blood pressure control; hormone
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;95-146/Product: adrenomedullin #status experimental <MAT>
F;147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following glyc
F;110-115/Disulfide bonds: #status experimental
F;146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 28.5%; Score 72.5; DB 2; Length 185;
Best Local Similarity 38.5%; Pred. No. 0.037;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

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Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146
```

RESULT 2
S41600
adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA enco
A;Reference number: S41600; MUID:94139945; PMID:8043068
A;Accession: S41600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-188 <KIT>
A;Cross-references: UNIPROT:P53366; GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379

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  Query Match           27.8%;  Score 70.5;  DB 2;  Length 188;
  Best Local Similarity  38.5%;  Pred. No. 0.069;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      :    ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDGVAPRSKISPQGY 146
```

RESULT 3
JN0766
adrenomedullin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
A;Reference number: JN0766; MUID:93384621; PMID:7690563
A;Accession: JN0766
A;Molecule type: mRNA
A;Residues: 1-185 <SAK>
A;Cross-references: UNIPROT:P43145
A;Accession: PN0610
A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
C;Keywords: amidated carboxyl end
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;94-143/Product: adrenomedullin #status predicted <MAT>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl

```
  Query Match           27.4%;  Score 69.5;  DB 2;  Length 185;
  Best Local Similarity  35.9%;  Pred. No. 0.092;
  Matches   14;  Conservative    7;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| :| |:|:::|      :   || :  ||  |
Db        106 GCRFGTCTMQKLAHQIYQFT-DKDKDGMAPRNKISPQGY 143
```

RESULT 4
AC3406
l-lactate permease [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3406
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <KUR>
A;Cross-references: UNIPROT:Q8YGC6; GB:AE008917; PIDN:AAL52414.1; PID:g17983216; GSPDB:GN
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1233
A;Map position: I

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  Query Match           22.8%;  Score 58;  DB 2;  Length 339;
  Best Local Similarity  27.7%;  Pred. No. 5.9;
  Matches   13;  Conservative    6;  Mismatches   20;  Indels    8;  Gaps    1;

Qy          8 VGCVLGTCQVQNLS--------HRLWQLMGPAGRQDSAPVDPSSPHS 46
              |  :   | :  |:         |:|    |  | : :||| |   ||
Db         31 VDVIAAICSMAALAAFLRFWQPRRIWTSTGKEGEETNAPVQPRHSHS 77
```

RESULT 5
A38731
alpha-1A adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A38731; A53280
R;Lomasney, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Feng, T.L.;
J. Biol. Chem. 266, 6365-6369, 1991
A;Title: Molecular cloning and expression of the cDNA for the alpha-1A-adrenergic recepto
A;Reference number: A38731; MUID:91177889; PMID:1706716
A;Accession: A38731
A;Molecule type: mRNA
A;Residues: 1-560 <LOM>
A;Cross-references: UNIPROT:P23944; GB:M60654; NID:g202761; PIDN:AAA63477.1; PID:g202762
R;Perez, D.M.; Piascik, M.T.; Graham, R.M.
Mol. Pharmacol. 40, 876-883, 1991
A;Title: Solution-phase library screening for the identification of rare clones: isolatic
A;Reference number: A53280; MUID:92100054; PMID:1661838
A;Accession: A53280
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-36,'P',38-58,'I',60-202,'I',204-305,'R',307-366,'I',368-370,'I',372-559 <PE
A;Experimental source: hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:73541)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

```
  Query Match           22.8%;  Score 58;  DB 2;  Length 560;
  Best Local Similarity  30.9%;  Pred. No. 10;
  Matches   17;  Conservative    3;  Mismatches   15;  Indels   20;  Gaps    2;

Qy          4 QLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQD------------SAPVDPSSPH 45
              :|||       || :    ||| |  |    |              :|  |||||
Db        409 RLLR-------CQCRRRRRRLWSLRPPLASLDRRRAFRLRPQPSHRSPRGPSSPH 456
```

RESULT 6
T29482
hypothetical protein F08B4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29482
R;Stellyes, L.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F08B4.
A;Reference number: Z20625
A;Accession: T29482
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

```
A;Residues: 1-1544 <STE>
A;Cross-references: UNIPROT:Q19194; EMBL:U52002; PIDN:AAB37728.1; GSPDB:GN00022; CESP:F0
A;Experimental source: strain Bristol N2; clone F08B4
C;Genetics:
A;Gene: CESP:F08B4.2
A;Map position: 4
A;Introns: 25/3; 74/3; 147/3; 238/1; 290/2; 391/2; 452/3; 526/3; 670/3; 734/1; 779/3; 83

  Query Match             22.8%;  Score 58;  DB 2;  Length 1544;
  Best Local Similarity   25.4%;  Pred. No. 30;
  Matches   15;  Conservative    7;  Mismatches   23;  Indels   14;  Gaps    1;

Qy          3 AQLLRVGCVLGTCQV-------------QNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              |  : :| .::| | |               | ||   | :||         ||| : : |
Db       1275 AVTVALGAIIGICAVCVFWSRYKTAQRNASNFSHSYPQKLGPIYHPTMMGVDPRTEYDY 1333


RESULT 7
T02844
cdc16-related protein, L3169.1 [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: H81461; T02844
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: H81461
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1784 <PYL>
A;Cross-references: UNIPROT:Q94606; GB:AE001274; NID:g3264850; PIDN:AAC24667.1; PID:g326
A;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
A;Gene: L3169.1
A;Map position: 1

  Query Match             22.4%;  Score 57;  DB 2;  Length 1784;
  Best Local Similarity   52.6%;  Pred. No. 47;
  Matches   10;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         16 QVQNLSHRLWQLMGPAGRQ 34
              ::|:| | ||:|:| | ||
Db        321 ELQHLWHTLWELLGAAWRQ 339


RESULT 8
E82662
ABC transporter ATP-binding protein XF1602 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82662
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-283 <SIM>
A;Cross-references: UNIPROT:Q9PD02; GB:AE003987; GB:AE003849; NID:g9106634; PIDN:AAF8441
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1602

  Query Match             21.3%;  Score 54;  DB 2;  Length 283;
  Best Local Similarity   34.1%;  Pred. No. 17;
  Matches   15;  Conservative    7;  Mismatches   18;  Indels    4;  Gaps    1;

Qy          1 TQAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSA----PVD 40
              |    :| | ::    ||||: |  ||:    : |||    |:|
Db        195 TDVMFIRDGHLVLNTDVQNLAKRYTQLLVDTDKLDSARALGPID 238


RESULT 9
T26050
hypothetical protein W01C9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26050
R;Sims, M.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z20143
A;Accession: T26050
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-792 <WIL>
A;Cross-references: UNIPROT:Q23115; EMBL:Z49969; PIDN:CAA90267.1; GSPDB:GN00020; CESP:W0
A;Experimental source: clone W01C9
C;Genetics:
A;Gene: CESP:W01C9.3
A;Map position: 2
A;Introns: 15/1; 40/1; 66/3; 101/3; 182/2; 270/3; 338/3; 366/1; 597/3; 613/2; 646/2; 684,

  Query Match             21.3%;  Score 54;  DB 2;  Length 792;
  Best Local Similarity   39.5%;  Pred. No. 50;
  Matches   15;  Conservative    3;  Mismatches   18;  Indels    2;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAG--RQDSAPVDPSSP 44
              | |        |||| |||| :   | |  ||: : |
Db        736 GLALENRDADGFSHRLQQLMGTSSNYRPDVEPVNYNVP 773


RESULT 10
A43708
gamma-interferon-inducible protein IP-30 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A43708
R;Luster, A.D.; Weinshank, R.L.; Feinman, R.; Ravetch, J.V.
J. Biol. Chem. 263, 12036-12043, 1988
A;Title: Molecular and biochemical characterization of a novel gamma-interferon-inducible
A;Reference number: A43708; MUID:88298888; PMID:3136170
A;Accession: A43708
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-303 <LUS>
A;Cross-references: UNIPROT:P13284; EMBL:J03909; NID:g186264; PIDN:AAA36105.1; PID:g3070

  Query Match             21.1%;  Score 53.5;  DB 2;  Length 303;
  Best Local Similarity   41.4%;  Pred. No. 21;
  Matches   12;  Conservative    3;  Mismatches   11;  Indels    3;  Gaps    1;

Qy         10 CVLGTCQVQNLSHRLWQLMGPAGRQDSAP 38
              |   | :|  | || |: :   || | ||
Db        209 CSPATARVCALGHRQWETL---GRSDPAP 234


RESULT 11
A37845
carboxylesterase (EC 3.1.1.1) precursor - Streptomyces scabies
```

```
C;Species: Streptomyces scabies
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
C;Accession: A37845; PC1103
R;Raymer, G.; Willard, J.M.A.; Schottel, J.L.
J. Bacteriol. 172, 7020-7026, 1990
A;Title: Cloning, sequencing, and regulation of expression of an extracellular esterase
A;Reference number: A37845; MUID:91072254; PMID:2254271
A;Accession: A37845
A;Molecule type: DNA
A;Residues: 1-345 <RAY>
A;Cross-references: UNIPROT:P22266; GB:M57297; NID:g153254; PIDN:AAA26743.1; PID:g153255
R;Schottel, J.L.; Hale, V.; Babcock, M.J.
Gene 115, 27-31, 1992
A;Title: Regulation and secretion of an extracellular esterase from Streptomyces scabies
A;Reference number: PC1103; MUID:92307438; PMID:1612447
A;Accession: PC1103
A;Molecule type: DNA
A;Residues: 1-54 <SCH>
A;Cross-references: GB:M57297
C;Comment: This protein is involved in suberin degradation.
C;Genetics:
A;Gene: est
C;Keywords: carboxylic ester hydrolase
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-345/Product: carboxylesterase #status predicted <MAT>

  Query Match             21.1%;  Score 53.5;  DB 2;  Length 345;
  Best Local Similarity   34.2%;  Pred. No. 24;
  Matches   13;  Conservative    3;  Mismatches   13;  Indels    9;  Gaps    1;

Qy          4 QLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDP 41
              :|      ||:|           | ||||   :|| ||
Db         16 RLTAAAVALGSCLA---------LAGPAGSAGAAPADP 44


RESULT 12
T35335
hypothetical protein SC5H1.19c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35335
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z21575
A;Accession: T35335
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <OLI>
A;Cross-references: UNIPROT:Q9X7S7; EMBL:AL049863; PIDN:CAB42944.1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC5H1.19c

  Query Match             20.9%;  Score 53;  DB 2;  Length 136;
  Best Local Similarity   38.1%;  Pred. No. 10;
  Matches   16;  Conservative    3;  Mismatches   19;  Indels    4;  Gaps    1;

Qy          7 RVGCVLGTCQVQNLSHRLWQL----MGPAGRQDSAPVDPSSP 44
              |:|  ||| :   |:  || |    |  | | |  |  |  |
Db         19 RIGVPLGTYRAPTLALALWWLRDRAMWIAERLDPQPDTPHLP 60


RESULT 13
AE2414
hypothetical protein all4869 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2414
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2414
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <KUR>
A;Cross-references: UNIPROT:Q8YMR4; GB:BA000019; PIDN:BAB76568.1; PID:g17134006; GSPDB:GN
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4869
C;Superfamily: Synechocystis hypothetical protein slr1160

  Query Match             20.9%;  Score 53;  DB 2;  Length 192;
  Best Local Similarity   40.0%;  Pred. No. 15;
  Matches    8;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         27 LMGPAGRQDSAPVDPSSPHS 46
              |: |   |:  |:||:||::
Db         23 LLAPVNAQNPQPIDPNSPNN 42


RESULT 14
H95954
probable Sir2-like transcription silencer protein [imported] - Sinorhizobium meliloti (st
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95954
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: H95954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-272 <KUR>
A;Cross-references: UNIPROT:P96452; GB:AL591985; PIDN:CAC49304.1; PID:g15140790; GSPDB:GN
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb21328
A;Genome: plasmid
C;Superfamily: uncharacterized conserved protein with Sir2 domain

  Query Match             20.9%;  Score 53;  DB 2;  Length 272;
  Best Local Similarity   26.1%;  Pred. No. 22;
  Matches   12;  Conservative   10;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          2 QAQLLRVGCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              :| :| :|  :    :: | ||:| :   :| :   |  ||    |
Db        187 EATVLFIGYSMSDLNIRLLLHRIWSIWRRSGHEKDRP--PSYVFMY 230


RESULT 15
E97187
dTDP-D-glucose 4,6-dehydratase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97187
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E97187
A;Status: preliminary
A;Molecule type: DNA
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A;Residues: 1-351 <KUR>
A;Cross-references: UNIPROT:Q97GN4; GB:AE001437; PIDN:AAK80288.1; PID:g15025341; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2332
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology

Query Match 20.9%; Score 53; DB 2; Length 351;
Best Local Similarity 22.4%; Pred. No. 28;
Matches 13; Conservative 12; Mismatches 11; Indels 22; Gaps 2;

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Qy          11 VLGTCQVQNLSHRLW-----------------QLMGPAGRQ----DSAPVDPSSPHS 46
               ||||  : |::   |                 :: |  |::    :: |::| ||:|
Db         103 VLGTVNLLNIAKNNWETKDGFKAGKKYLQISTDEVYGSLGKEGFFTETTPLNPHSPYS 160
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Search completed: May 4, 2005, 18:14:56
Job time : 41 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2005, 18:06:10 ; Search time 41 Seconds
(without alignments)
85.573 Million cell updates/sec

Title: US-10-723-368-5
Perfect score: 254
Sequence: 1 TQAQLLRVGCVLGTCQVQNL.....MGPAGRQDSAPVDPSSPHSY 47

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	72.5	28.5	38	4	US-09-280-501-6	Sequence 6, Appli
2	72.5	28.5	40	4	US-09-280-501-11	Sequence 11, Appl
3	72.5	28.5	52	3	US-09-070-504-14	Sequence 14, Appl
4	72.5	28.5	52	4	US-09-813-345C-14	Sequence 14, Appl
5	72.5	28.5	185	1	US-08-233-389C-1	Sequence 1, Appli
6	72.5	28.5	185	2	US-08-801-863-1	Sequence 1, Appli
7	72.5	28.5	185	2	US-08-486-596A-1	Sequence 1, Appli
8	72.5	28.5	185	2	US-09-004-713-1	Sequence 1, Appli
9	70.5	27.8	188	1	US-08-233-389C-3	Sequence 3, Appli
10	70.5	27.8	188	2	US-08-801-863-3	Sequence 3, Appli
11	70.5	27.8	188	2	US-08-486-596A-3	Sequence 3, Appli
12	70.5	27.8	188	2	US-09-004-713-3	Sequence 3, Appli
13	69.5	27.4	50	3	US-09-070-504-15	Sequence 15, Appl
14	69.5	27.4	50	4	US-09-813-345C-15	Sequence 15, Appl
15	65.5	25.8	40	4	US-09-280-501-8	Sequence 8, Appli
16	65.5	25.8	50	4	US-09-280-501-7	Sequence 7, Appli
17	58	22.8	559	2	US-08-406-855A-20	Sequence 20, Appl
18	58	22.8	559	3	US-09-206-899-20	Sequence 20, Appl
19	58	22.8	560	4	US-09-688-415-8	Sequence 8, Appli
20	56	22.0	172	4	US-09-949-016-9374	Sequence 9374, Ap
21	56	22.0	770	4	US-09-252-991A-28510	Sequence 28510, A
22	55.5	21.9	906	4	US-09-252-991A-22132	Sequence 22132, A
23	54.5	21.5	184	4	US-09-252-991A-32339	Sequence 32339, A
24	54	21.3	133	4	US-09-252-991A-30594	Sequence 30594, A
25	53.5	21.1	218	4	US-09-270-767-43455	Sequence 43455, A
26	53.5	21.1	303	4	US-09-949-016-6717	Sequence 6717, Ap
27	53	20.9	181	4	US-09-530-685A-21	Sequence 21, Appl
28	53	20.9	239	4	US-09-530-685A-32	Sequence 32, Appl
29	53	20.9	255	4	US-09-902-540-14178	Sequence 14178, A
30	53	20.9	309	4	US-09-530-685A-31	Sequence 31, Appl
31	53	20.9	450	3	US-09-120-365-68	Sequence 68, Appl
32	53	20.9	450	3	US-09-515-039-68	Sequence 68, Appl
33	53	20.9	605	3	US-08-753-007A-2	Sequence 2, Appli
34	53	20.9	605	3	US-09-398-496-2	Sequence 2, Appli
35	53	20.9	754	2	US-08-525-864A-2	Sequence 2, Appli
36	52	20.5	263	4	US-09-270-767-46206	Sequence 46206, A
37	52	20.5	675	4	US-09-252-991A-32681	Sequence 32681, A
38	52	20.5	3898	3	US-08-750-717-2	Sequence 2, Appli
39	51.5	20.3	149	4	US-09-543-681A-8072	Sequence 8072, Ap
40	51.5	20.3	155	4	US-09-252-991A-20281	Sequence 20281, A
41	51.5	20.3	220	4	US-09-902-540-11202	Sequence 11202, A
42	51.5	20.3	879	4	US-09-252-991A-31990	Sequence 31990, A
43	51	20.1	1213	2	US-08-937-102-2	Sequence 2, Appli
44	51	20.1	1399	4	US-09-388-221B-4	Sequence 4, Appli
45	51	20.1	1424	4	US-09-388-221B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-280-501-6
; Sequence 6, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-6

Query Match 28.5%; Score 72.5; DB 4; Length 38;
Best Local Similarity 38.5%; Pred. No. 0.0098;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```
Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db          1 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 38
```

RESULT 2
US-09-280-501-11
; Sequence 11, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11

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;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-11

  Query Match             28.5%;  Score 72.5;  DB 4;  Length 40;
  Best Local Similarity   38.5%;  Pred. No. 0.01;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| ||  |:|:::|      : : ||    ||  |
Db          3 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 40


RESULT 3
US-09-070-504-14
; Sequence 14, Application US/09070504
; Patent No. 6268474
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Derek D.
;    APPLICANT:  Saha, Shankar
;    APPLICANT:  Abel, Peter W.
;    TITLE OF INVENTION:  PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;    TITLE OF INVENTION:  SUPERFAMILY AND METHODS OF USE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch & Gebhardt, P.A.
;      STREET:  119 No. 6268474th Fourth Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/070,504
;      FILING DATE:  30-APR-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McCormack, Myra H
;      REGISTRATION NUMBER:  36,602
;      REFERENCE/DOCKET NUMBER:  180.00020101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/305-1220
;      TELEFAX:  612/305-1228
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-070-504-14

  Query Match             28.5%;  Score 72.5;  DB 3;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.014;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| ||  |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 4
US-09-813-345C-14
; Sequence 14, Application US/09813345C
; Patent No. 6756205
; GENERAL INFORMATION:
;  APPLICANT: CREIGHTON UNIVERSITY
;  APPLICANT:  SMITH, Derek D.
;  APPLICANT:  SAHA, Shankar
;  APPLICANT:  ABEL, Peter W.
;  TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: 180.00020102
;  CURRENT APPLICATION NUMBER: US/09/813,345C
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: 09/070,504
;  PRIOR FILING DATE: 1998-04-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially Synthesized Peptide
US-09-813-345C-14

  Query Match             28.5%;  Score 72.5;  DB 4;  Length 52;
  Best Local Similarity   38.5%;  Pred. No. 0.014;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| ||  |:|:::|      : : ||    ||  |
Db         15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 52


RESULT 5
US-08-233-389C-1
; Sequence 1, Application US/08233389C
; Patent No. 5639855
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,389C
;      FILING DATE:  26-APR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  185 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-233-389C-1

  Query Match             28.5%;  Score 72.5;  DB 1;  Length 185;
  Best Local Similarity   38.5%;  Pred. No. 0.056;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;
```

```
Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| ||  |:|:::|      : : ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146


RESULT 6
US-08-801-863-1
; Sequence 1, Application US/08801863
; Patent No. 5830703
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,863
;      FILING DATE:  CONCURRENTLY HEREWITH
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5 DIV3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  185 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-801-863-1

  Query Match             28.5%;  Score 72.5;  DB 2;  Length 185;
  Best Local Similarity   38.5%;  Pred. No. 0.056;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| ||  |:|:::|      : : ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146


RESULT 7
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,596A
;      FILING DATE:  JUNE 7, 1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5 DIV1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  185 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-486-596A-1

  Query Match             28.5%;  Score 72.5;  DB 2;  Length 185;
  Best Local Similarity   38.5%;  Pred. No. 0.056;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| ||  |:|:::|      : : ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146


RESULT 8
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/004,713
;      FILING DATE:  JANUARY 7, 1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5 DIV2 CON
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  185 amino acids
;      TYPE:  amino acid
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-004-713-1

  Query Match                 28.5%;  Score 72.5;  DB 2;  Length 185;
  Best Local Similarity   38.5%;  Pred. No. 0.056;
  Matches   15;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      : : ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPQGY 146


RESULT 9
US-08-233-389C-3
; Sequence 3, Application US/08233389C
; Patent No. 5639855
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,389C
;      FILING DATE:  26-APR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  188 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-233-389C-3

  Query Match                 27.8%;  Score 70.5;  DB 1;  Length 188;
  Best Local Similarity   38.5%;  Pred. No. 0.11;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      :   ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDGVAPRSKISPQGY 146


RESULT 10
US-08-801-863-3
; Sequence 3, Application US/08801863
; Patent No. 5830703
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,863
;      FILING DATE:  CONCURRENTLY HEREWITH
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5 DIV3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  188 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-801-863-3

  Query Match                 27.8%;  Score 70.5;  DB 2;  Length 188;
  Best Local Similarity   38.5%;  Pred. No. 0.11;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      :   ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDGVAPRSKISPQGY 146


RESULT 11
US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,596A
;      FILING DATE:  JUNE 7, 1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5 DIV1
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  188 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-486-596A-3

  Query Match             27.8%;  Score 70.5;  DB 2;  Length 188;
  Best Local Similarity   38.5%;  Pred. No. 0.11;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      :   ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDGVAPRSKISPQGY 146


RESULT 12
US-09-004-713-3
; Sequence 3, Application US/09004713
; Patent No. 5910416
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/004,713
;      FILING DATE:  JANUARY 7, 1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5 DIV2 CON
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  188 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-004-713-3

  Query Match             27.8%;  Score 70.5;  DB 2;  Length 188;
  Best Local Similarity   38.5%;  Pred. No. 0.11;
  Matches   15;  Conservative    5;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| || |:|:::|      :   ||    ||  |
Db        109 GCRFGTCTVQKLAHQIYQFT-DKDKDGVAPRSKISPQGY 146


RESULT 13
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Derek D.
;    APPLICANT:  Saha, Shankar
;    APPLICANT:  Abel, Peter W.
;    TITLE OF INVENTION:  PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;    TITLE OF INVENTION:  SUPERFAMILY AND METHODS OF USE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch & Gebhardt, P.A.
;      STREET:  119 No. 6268474th Fourth Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/070,504
;      FILING DATE:  30-APR-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McCormack, Myra H
;      REGISTRATION NUMBER:  36,602
;      REFERENCE/DOCKET NUMBER:  180.00020101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/305-1220
;      TELEFAX:  612/305-1228
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-070-504-15

  Query Match             27.4%;  Score 69.5;  DB 3;  Length 50;
  Best Local Similarity   35.9%;  Pred. No. 0.033;
  Matches   14;  Conservative    7;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSPHSY 47
              ||  ||| :| |:|:::|      :   || :  ||  |
Db         13 GCRFGTCTMQKLAHQIYQFT-DKDKDGMAPRNKISPQGY 50


RESULT 14
US-09-813-345C-15
; Sequence 15, Application US/09813345C
; Patent No. 6756205
; GENERAL INFORMATION:
;  APPLICANT: CREIGHTON UNIVERSITY
;  APPLICANT:  SMITH, Derek D.
;  APPLICANT:  SAHA, Shankar
;  APPLICANT:  ABEL, Peter W.
;  TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: 180.00020102
;  CURRENT APPLICATION NUMBER: US/09/813,345C
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: 09/070,504
;  PRIOR FILING DATE: 1998-04-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
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; OTHER INFORMATION: Artificially Synthesized Peptide
US-09-813-345C-15

Query Match 27.4%; Score 69.5; DB 4; Length 50;
Best Local Similarity 35.9%; Pred. No. 0.033;
Matches 14; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

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Db         13 GCRFGTCTMQKLAHQIYQFT-DKDKDGMAPRNKISPQGY 50
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RESULT 15
US-09-280-501-8
; Sequence 8, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-8

Query Match 25.8%; Score 65.5; DB 4; Length 40;
Best Local Similarity 38.9%; Pred. No. 0.089;
Matches 14; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

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Qy          9 GCVLGTCQVQNLSHRLWQLMGPAGRQDSAPVDPSSP 44
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Db          5 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISP 39
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Search completed: May 4, 2005, 18:15:51
Job time : 50 secs